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QY 1158 CTACTCAGCTGACCTGTCTCATCCCATTTGCGCGAGAGTGAACGTCGCCACCTCTCT 1217
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QY 2178 CCCATCAGGACATAGGGGCAACCTCAGGGCTTCAAGCAGCTTCCATCCATCTGTGGCCA 2237
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QY 2298 TTTCTGCGCACCCCAAGCAGAGGTTTCTGCCCCCAGAGGGCTGAGCCGCCACCCAGCAGT 2357
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Db 2601 CTTTGCCTTTGGTGGAGATGCAAGGGGCTGCTGCGGCGAGGGGCCCATGTTGGGCCAGGAT 2660
QY 2838 AGCTTGGGCTGTCTCCAGTGGAGGAGAGAGCAGGAGAGCGGCTGAGTCCCA 2897
Db 2661 AGCTTGGGCTGTCTCCAGTGGAGGAGAGAGCAGGAGAGCGGCTGAGTCCCA 2720
QY 2898 GTGCGAGGAGCAGCAGGAGGCGCAGGCTGAGAGCCCACTGCCCCCAGGTCAAGTCAAGGCC 2957
Db 2721 GTGCGAGGAGCAGCAGGAGGCGCAGGCTGAGAGCCCACTGCCCCCAGGTCAAGTCAAGGCC 2780
QY 2958 TGTGCTTGGGCTGGGCGAGGCTCCCAAGGAGCTCTCCAGAGGCCCAACCCCATGGGAGGA 3017
Db 2781 TGTGCTTGGGCTGGGCGAGGCTCCCAAGGAGCTCTCCAGAGGCCCAACCCCATGGGAGGA 2840
QY 3018 CATCGGCGAGGCTCTCCCTGCTGAGATCCGGGACCTTGTCTGAGGTGATGCGAGGCGGCGCA 3077
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QY 3138 CGATATCAAGTACTCTCCCATTCGAGTTTATGATCTTTCAGGAAAGTCCCCCAAGTCCGCTCA 3197
Db 2961 CGATATCAAGTACTCTCCCATTCGAGTTTATGATCTTTCAGGAAAGTCCCCCAAGTCCGCTCA 3020
QY 3198 GCGAGGCGGCTCTCCCTGCTGAGGAGGAGCTGCGGCGAGTTCGCCGAGGCCACGCTG 3257

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	DB	GCCTGGCCAGGTGAACTGGGCCCCCACGACGGCCCTGGAGATCAAGAGAGTCAAGAGGA	3140
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3438	QY	GCTGCGTAGAGAGTGAAGGCTTCGTGGAGACATCTCCGGAATCTGAAGGCGCAGGCC	3497
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3501	DB	GGCCACCTGGAGCAAGAGACGGAGCCCTCTGGAGAGCAGCAGCGTGTCTCATCTCTGC	3560
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3561	DB	CACCTCAGAACTTTCAGGTTCTGACCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3620
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4038	QY	CAGCAAGCTCTCCCGGGGTGGCACCTTACCTTCGCGACGGCATGTGTACGCAAGGCAGG	4097
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4098	QY	AATGGGTCCCTACAGCAGCCCTCGGAGCGAGTCTCTCTGGGGGCGCCAGCCACTGGC	4157
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4158	QY	CTCTGAGGAGGAGCAGGGCGGTTCAGCCCAACCCCTGCGCCAGCAAAAGACCTTCGC	4217
3981	DB	CTCTGAGGAGGAGCAGGGCGGTTCAGCCCAACCCCTGCGCCAGCAAAAGACCTTCGC	4040
4218	QY	ATTCCAGACACAGATCCAGAGGGCGCTTACGCGTGTGTGGGCAATGTCTGGGAGAGGC	4277
4041	DB	ATTCCAGACACAGATCCAGAGGGCGCTTACGCGTGTGTGGGCAATGTCTGGGAGAGGC	4100
4278	QY	CAGCGGCGGGCGCTGCGGCCCAAGATCATCCCTTACACCCCAAGACAGACGAGT	4337
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RESULT 7

AAC62287

AAC62287
ID AAC62287 standard: cDNA: 7928 BP.XX
ID
FACB

AAC62287:

AC
YY
HACB

XX DT 19-MAR-2007 (first entry)

DT 19-N
vvy

DE cDNA encoding a snlice variant of a signal transduction polypeptide.

DE yy
cdNA encoding a splice variant of a signal transduction polypeptide.

XX
XX

~~Tue~~

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 06:40:08 ; Search time 13028 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18	639.8	12.3	250087	2	AC096931	AC096931 Rattus no
19	613.8	11.8	164766	2	AC026657	AC026657 Homo sapi
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44	173.4	3.3	2224	6	BD012208	BD012208 Novel Gen
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ALIGNMENTS

RESULT 1
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LOCUS AR255867 5207 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6482624.
ACCESSION AR255867
VERSION AR255867.1 GI:27305065
KEYWORDS
SOURCE Unknown.
ORGANISM Unknwn.
REFERENCE 1 (bases 1 to 5207)
AUTHORS Wei,M.-H., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL Patent: US 6482624-A 1 19-NOV-2002;

Pred. No. is the number of results predicted by chance to have a

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	/mol_type="genomic DNA"		
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Best Local Similarity	100.0%;	Prd. No. 0;	
Matches 5207;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Db	1	CAGCACGAGGAATCCTTCTCTATCCTCTGGCCAGCTCAGATCAGAGTGGGAGAGGCAGTG	60
OY	61	GTTCATTGAAGAGTACTCCTTAATGTCAGAACCTGGGCGGTTCAGATGGGAGTGGTCTGT	120
Db	61	GTTCATTGAAGAGTACTCCTTAATGTCAGAACCTGGGCGGTTCAGATGGGAGTGGTCTGT	120
OY	121	CGCTTGGGCTCGGGGGGTGTTCAAGTGCACAGTGTATCTCAGGGTCTCACCAACCAT	180
Db	121	CGCTTGGGCTCGGGGGGTGTTCAAGTGCACAGTGTATCTCAGGGTCTCACCAACCAT	180
OY	181	CAAAGCATGGTAGGCTGTGGCTGGCACCCAGAGGTGTGTGGCTGGGAGTGGTCTCCAC	240
Db	181	CAAAGCATGGTAGGCTGTGGCTGGCACCCAGAGGTGTGTGGCTGGGAGTGGTCTCCAC	240
OY	241	AGTTCCCTCCCTGGCTCCAGGGGCCCATTCATGAGGTAAACATTCGAGGATGTGCA	300
Db	241	AGTTCCCTCCCTGGCTCCAGGGGCCCATTCATGAGGTAAACATTCGAGGATGTGCA	300
OY	301	GCACAGACAGCGCGGAAACGGGCCCAATTCAGAGGCTATCATTCAGGGCCACCAACAGCCCTCG	360
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OY	361	GTGACCTGGTACAGGACAGGCTCCAGCTGGTGCACAGCACCCGGCTTAGCAGAGCA	420
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OY	481	ACCTGCTGGCCCAACACATGTTGGCAGGTGCTGTGCAGGCAGAGCTGTGTGCTT	540
Db	481	ACCTGCTGGCCCAACACATGTTGGCAGGTGCTGTGCAGGCAGAGCTGTGTGCTT	540
OY	541	GGGGGGACAATGAGCCGGAATCAGAGAAGCAAGCCACCGGAGGAAGCTGCACCTCTTC	600
Db	541	GGGGGGACAATGAGCCGGAATCAGAGAAGCAAGCCACCGGAGGAAGCTGCACCTCTTC	600
OY	601	TATGAGTTCAGAGGAGGATTTGAAGGGGCGCTTTGGCTTCGTAAGAAGCTGCAGAC	660
Db	601	TATGAGTTCAGAGGAGGATTTGAAGGGGCGCTTTGGCTTCGTAAGAAGCTGCAGAC	660
OY	661	AAAGGAACCAAGATCTTTGCGCTGCCAAGTTCATCCCTCTACGGAGCAGAACTCGGGCC	720
Db	661	AAAGGAACCAAGATCTTTGCGCTGCCAAGTTCATCCCTCTACGGAGCAGAACTCGGGCC	720
OY	721	CAGGCATACAGGAGCGAGACATCTGGCGCGCTGAGCCACCCGCTGTGTACGGGGCTG	780
Db	721	CAGGCATACAGGAGCGAGACATCTGGCGCGCTGAGCCACCCGCTGTGTACGGGGCTG	780
OY	781	CTGACCAGTTTGAGACCCCAAGACCTCATCCTCATCCTGAGAGTGTGTCTATCCCGAG	840
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OY	841	GAGTGTGTGACCGCTGTACAGGAAGGGCGTGGTGAAGGAGGCGTGGTCAAGGTCTAC	900
Db	841	GAGTGTGTGACCGCTGTACAGGAAGGGCGTGGTGAAGGAGGCGTGGTCAAGGTCTAC	900
OY	901	ATCAGCAGCTGTGGAGGGGTGCACTACCTGCAAGCCATGTGGCGTCTCCACTGAGC	960
Db	901	ATCAGCAGCTGTGGAGGGGTGCACTACCTGCAAGCCATGTGGCGTCTCCACTGAGC	960

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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1
Ketchum K., Beasley, E.M., Wei, M.H. and di Francesco, V.
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DEFINITION Sequence 3 from Patent WO240683.
ACCESSION AX430858
VERSION AX430858.1 GI:21655922
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE Ketchum, K., Beasley, E.M., Wei, M.H. and di Francesco, V.
AUTHORS Isolated human kinase proteins, nucleic acid molecules encoding
TITLE human kinase proteins, and uses thereof
JOURNAL Patent: WO 0240683-A 3 23-MAY-2002;
PE CORP NY (US)
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QY 541 GGGGGGGAACAATGAGCCGCTCAGAGAGAGAAAGCCACCGAGGAGTGCATCCCTTC 600
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QY 601 TATAGGTCAAGAGAGATTTGAAAGGGCGTGTGGCTTCTGTAATAAAGAGTGCAGAC 660
Db 601 TATAGGTCAAGAGAGATTTGAAAGGGCGTGTGTGGCTTCTGTAATAAAGAGTGCAGAC 660
QY 661 AAAGGAAACAGATCTTGTGCGCTGCCAAGTTTCATCCCTACGGAGCAGAACTCGGGCC 720
Db 661 AAAGGAAACAGATCTTGTGCGCTGCCAAGTTTCATCCCTACGGAGCAGAACTCGGGCC 720
QY 721 CAGGCATACAGGAGGAGAGATCTTGTGCGCGCTGAGCCACCGCTGTGTCAGGGGCTG 780
Db 721 CAGGCATACAGGAGGAGAGATCTTGTGCGCGCTGAGCCACCGCTGTGTCAGGGGCTG 780
QY 781 CTGGACCACTTTGAGACCGCAAGACCTCTCATCTCTGAGAGTGTGCTCATCCGAG 840
Db 781 CTGGACCACTTTGAGACCGCAAGACCTCTCATCTCTGAGAGTGTGCTCATCCGAG 840
QY 841 GAGTCTCTGAGCGCGCTGTACAGGAGGCGTGTGTAACGAGGCGAGTCAAGTCTAC 900
Db 841 GAGTCTCTGAGCGCGCTGTACAGGAGGCGTGTGTAACGAGGCGAGTCAAGTCTAC 900
QY 901 ATCCACAGCTGTGTGAGGGGCTGCATCTGTCACAGCATGCGGTCTTCCACCTGGAC 960
Db 901 ATCCACAGCTGTGTGAGGGGCTGCATCTGTCACAGCATGCGGTCTTCCACCTGGAC 960
QY 961 ATAAAGCCCTCTAAACATCTGATGTGTCATCTGTCGCGGGAAGACATTAATAATCTCGAC 1020
Db 961 ATAAAGCCCTCTAAACATCTGATGTGTCATCTGTCGCGGGAAGACATTAATAATCTCGAC 1020
QY 1021 TTTGGCTTTGCCAGAACATCACCCAGCAGAGCTGACGTCAGCCAGTACCGCTCCCT 1080
Db 1021 TTTGGCTTTGCCAGAACATCACCCAGCAGAGCTGACGTCAGCCAGTACCGCTCCCT 1080
QY 1081 GAGTTCGTCTCCCTCCAGATCATCCAGCAGAACCTGTGAGGAGAGCTCCGACATTTGG 1140
Db 1081 GAGTTCGTCTCCCTCCAGATCATCCAGCAGAACCTGTGAGGAGAGCTCCGACATTTGG 1140
QY 1141 GCATGGGTGTCTCTCTACCTGACCTGACCTGACCTGATCCCATTTGCGCGAGAGT 1200
Db 1141 GCATGGGTGTCTCTCTACCTGACCTGACCTGATCCCATTTGCGCGAGAGT 1200
QY 1201 GACCGTGCACACCTCTGAAACGTCCTGGAGGGCGGTGTCTATGAGAGACCCCATTTGG 1260
Db 1201 GACCGTGCACACCTCTGAAACGTCCTGGAGGGCGGTGTCTATGAGAGACCCCATTTGG 1260
QY 1261 GCGCACCTCAGCAGAACGCGCAAGATTCATCAGGCTACGCTGAGAGAGCCCTCAG 1320
Db 1261 GCGCACCTCAGCAGAACGCGCAAGATTCATCAGGCTACGCTGAGAGAGCCCTCAG 1320
QY 1321 GCGCGCTAGTGCAGCCAGTCCCTCTCCACCCCTGTTCTGAAATCCATGCTGG 1380
Db 1321 GCGCGCTAGTGCAGCCAGTCCCTCTCCACCCCTGTTCTGAAATCCATGCTGG 1380
QY 1381 GAGAGGCCCATTTATCAACACCAAGAGCTCAAGTTCCTCTGCGGAGTCTGCTG 1440
Db 1381 GAGAGGCCCATTTATCAACACCAAGAGCTCAAGTTCCTCTGCGGAGTCTGCTG 1440
QY 1441 CAGGTTCCCTGATGAGTACAGTCCATCTGATGCTGATGCTCCATCTGAGTGTG 1500
Db 1441 CAGGTTCCCTGATGAGTACAGTCCATCTGATGCTGATGCTCCATCTGAGTGTG 1500
QY 1501 CGGGGCCACCCGACAGCCCTCTCTGCGGTAGCCCGGACCTCTGAGGAGACATGGT 1560
Db 1501 CGGGGCCACCCGACAGCCCTCTCTGCGGTAGCCCGGACCTCTGAGGAGACATGGT 1560
QY 1561 GGCTCTCCAGTTCTCTCTCTCTGACACAGAGCTCGCCCATTTGCGCGGGTAA 1620
Db 1561 GGCTCTCCAGTTCTCTCTCTCTCTGACACAGAGCTCGCCCATTTGCGCGGGTAA 1620
QY 1621 TCACTGCACCCCTCCCGGTGACACATCACTACCTGCTGACCCCGGGGCTCTCTGCGG 1680
Db 1621 TCACTGCACCCCTCCCGGTGACACATCACTACCTGCTGACCCCGGGGCTCTCTGCGG 1680

Query Match	99.4%;	Score 5173.6;	DB 6;	Length 5454;
Best Local Similarity	99.8%;	Prod. No. 0;		
Matches 5179;	Conservative	0; Mismatches	9; Indels	0; Gaps
QY	3	GCACGAGGAACCTCCTTCTGATCACCTGGCCACGTGAGGT	CAGAGTGAGGAGAGCACTGGT	62
Db	267	GCCCACCAACTCCTTCTGATCACCTGGCCACGTGAGT	CAGAGTGAGGAGAGCACTGGT	326
QY	63	TCATTTGAGGAGTACTCTTACTGTCAGAACTCTGGCCGTCAGGATGGGGTCTGTCTG	122	
Db	327	TCATTTGAGGAGTACTCTTACTGTCAGAACTCTGGCCGTCAGGATGGGGTCTGTCTG	386	
QY	123	CTTGGGCTGGGGGGGTGTTCAATGTCGCCACAGTGTATCTCAAGGTCACCAACCATCC	182	
Db	387	CTTGGGCTGGGGGGGTGTTCAATGTTGCCACAGTGTATCTCAAGGTCACCAACCATCC	446	
QY	183	AAGCATGTTAGGCTGTGGCTGGCACCCACAGGGTCTGTGGCTGGGGAGGTGGTCTCCACAG	242	
Db	447	AAGCATGTTAGGCTGTGGCTGGCACCCACAGGGTCTGTGGCTGGGGAGGTGGTCTCCACAG	506	
QY	243	TTCCCTCCCTCCCTCCAGGGCCCCATCCATCAGGTTAACCATCGAGGATGTGCAGGC	302	
Db	507	TTCCCTCCCTCCCTCCAGGGCCCCATCCATCAGGTTAACCATCGAGGATGTGCAGGC	566	
QY	303	ACAGACAGCGGAAACGGCCCCAATTGAGGGCTATCATTTGAGGGGAGCCACAGCCCTCGGT	362	
Db	567	ACAGACAGCGGAAACGGCCCCAATTGAGGGCTATCATTTGAGGGGAGCCACAGCCCTCGGT	626	

QY	363	GACCTGGTACAAGGACAGCGTCCAGCTGGTGGACAGGACCCGGCTTTAGCCAGCAGCAAGA	432
Db	627	GACCTGGTACAAGGACAGCGTCCAGCTGGTGGACAGGACCCGGCTTTAGCCAGCAGCAAGA	686
QY	423	AGGCACCACTATCCCTTGGTGTGAGGCATGTGGGCTTCAAAGGATGCCGGCGTTTACAC	482
Db	687	AGGCACCACTATCCCTTGGTGTGAGGCATATGGCCTCGAAGGATGCCGGCGTTTACAC	746
QY	483	CTGCGCTGGCCCAAAACACTGGTGGCCAGGTGCTCTCAAGGCAGAGCTGCTGGTGGCTGG	542
Db	747	CTGCGCTGGCCCAAAACACTGGTGGCCAGGTGCTCTCAAGGCAGAGCTGCTGGTGGCTGG	806
QY	543	GGGGACCAATGAGCCGGACTCAGAGAGCAAGGCCACCGGAGGAAAGCTGCACCTCTTCTTA	602
Db	807	GGGGACCAATGAGCCGGACTCAGAGAGCAAGGCCACCGGAGGAAAGCTGCACCTCTTCTTA	866
QY	603	TGAGCTCAAGGAGGAGATTCGAGAGGGGCGTGTGGCTTCGTAAGAGGTGACAGCAAA	662
Db	867	TGAGGTCAAGGAGGAGATTCGAGAGGGGCGTGTGGCTTCGTAAGAGGTGACAGCAAA	926
QY	663	AGGAAACAAGATCTTTGGCGCTGCAAGTTCACTCCCTCTAGGAGCAGAACTCGGGGCCA	722
Db	927	AGGAAACAAGATCTTTGGCGCTGCAAGTTCACTCCCTCTAGGAGCAGAACTCGGGGCCA	986
QY	723	GGCATACAGGAGCGAGACATCTCTGGCGCGCTGAGCCACCGCTGGTGCACGGGGCTGTCT	782
Db	987	GGCATACAGGAGCGAGACATCTCTGGCGCGCTGAGCCACCGCTGGTGCACGGGGCTGTCT	1046
QY	783	GGACCGATTTAGACCCGCAAGACCTCATCTCATCTCTGAGCTGTGCTCATCCGAGGA	842
Db	1047	GGACCGATTTAGACCCGCAAGACCTCATCTCATCTCTGAGCTGTGCTCATCCGAGGA	1106
QY	843	GCTGCTGACCGCCTGTACAGGAAGGGCGTGTGACGGAGGCCAGGTCCTCAAGTGTCTACAT	902
Db	1107	GCTGCTGACCGCCTGTACAGGAAGGGCGTGTGACGGAGGCCAGGTCCTCAAGTGTCTACAT	1166
QY	903	CCAGCAGCTGGTGGAGGGGCTGACCTAGCTGCACAGCCATGGCGTCTCCACCTGACAT	962
Db	1167	CCAGCAGCTGGTGGAGGGGCTGACCTAGCTGCACAGCCATGGCGTCTCCACCTGACAT	1226
QY	963	AAAGCCCTTAACATCCTGTATGTGCATCTCTCCCGGGAAGACATTAATTTGCGACTT	1022
Db	1227	AAAGCCCTTAACATCCTGTATGTGTGCATCTCTCCCGGGAAGACATTAATTTGCGACTT	1286
QY	1023	TGGCTTTGCCCAGAAACATCACCCAGCAGAGTGCAGTTTCAGCCAGTACCGCTCCCTCGA	1082
Db	1287	TGGCTTTGCCCAGAAACATCACCCAGCAGAGTGCAGTTTCAGCCAGTACCGCTCCCTCGA	1346
QY	1083	GTTCGTCTCCCGGAGATCATCCAGCAGAACCTCTGAGCGAAGCTCCCGACATTTGGGC	1142
Db	1347	GTTCGTCTCCCGGAGATCATCCAGCAGAACCTCTGAGCGAAGCTCCCGACATTTGGGC	1406
QY	1143	CATGGTGTATCTCTTACCTCAGCCTGACCTGCTCATCCCATTTGCGCGCAGAGTGA	1202
Db	1407	CATGGTGTATCTCTTACCTCAGCCTGACCTGCTCATCCCATTTGCGCGCAGAGTGA	1466
QY	1203	CCGTGCCACCTCTCTGAAGCTCTGAGGGGGCGCTGTCTGAGAGCAGCCCTCATGGCTGC	1262
Db	1467	CCGTGCCACCTCTCTGAAGCTCTGAGGGGGCGCTGTCTGAGAGCAGCCCTCATGGCTGC	1526
QY	1263	CCACTCAGCGAAGACGCCAAAGCTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGC	1322
Db	1527	CCACTCAGCGAAGACGCCAAAGCTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGC	1586
QY	1323	CCGACCTAGTGGCGCCAGTGCCTCTCCACCCCTGGTTCCTGGAATTCATGCTCGGA	1382
Db	1587	CCGACCTAGTGGCGCCAGTGCCTCTCCACCCCTGGTTCCTGGAATTCATGCTCGGA	1646
QY	1383	GGAGGCCCATTTATCAACACCAAGCAGCTCAAGTTCTCTGGTGGCCGGAAGTCGCTGGCA	1442
Db	1647	GGAGGCCCATTTATCAACACCAAGCAGCTCAAGTTCTCTGGTGGCCGGAAGTCGCTGGCA	1706

QY	1443	GC	TTCCCTCGATGAGCTACAAAGTCCATCTCTGGTGTATGCGCTCCATCCCTGAGTGTCTGG	1501
DB	1707	GC	GTTCCTCTGATGAGCTACAAAGTCCATCTCTGGTGTATGCGCTCCATCCCTGAGTGTCTGG	1766
QY	1503	GG	GGCCACCCGACAGAGCCCTCCCTCGCGCTAGCCCGCACCTCTGCAGGAGCACTGGTGG	1562
DB	1767	GG	GGCCACCCGACAGAGCCCTCCCTCGCGCTAGCCCGCACCTCTGCAGGAGCACTGGTGG	1826
QY	1563	CT	CTCCAGATTCTCTCTCTCTCTGTGACAAAGAGCTCGCCCAATTTTCCCGGGCTTAAGTC	1622
DB	1827	CT	CTCCAGATTCTCTCTCTCTCTGTGACAAAGAGCTCGCCCAATTTTCCCGGGCTTAAGTC	1886
QY	1623	ACT	GCCACCTCCCGGTGACACACTCACCACCTGCTGCACCCCGGGGTTCCTCGCGGC	1682
DB	1887	ACT	GCCACCTCCCGGTGACACACTCACCACCTGCTGCACCCCGGGGTTCCTCGCGGC	1946
QY	1683	CT	GGCAGCGCTGCTGAGGAAGCGAGGCACTGAGCGTCCACGAGGCCCGCACTCC	1742
DB	1947	CT	GGCAGCGCTGCTGAGGAAGCGAGGCACTGAGCGTCCACGAGGCCCGCACTCC	2006
QY	1743	GC	CTGATCTCCGAGGGTCCGGGCGACCGGCGGCCAGAGGCTGCGTGCCTCCGCGCACAG	1802
DB	2007	GC	CTGATCTCCGAGGGTCCGGGCGACCGGCGGCCAGAGGCTGCGTGCCTCCGCGCACAG	2066
QY	1803	CG	TATCCGAGCGTGTCTTACACAGCGGGTGTAGGCCCTGAGCACGGGGCCCTGGC	1862
DB	2067	CG	TATCCGAGCGTGTCTTACACAGCGGGTGTAGGCCCTGAGCACGGGGCCCTGGC	2126
QY	1863	CC	GGGAGCAGCGGCACCCCGGCCGGCGGCACCTGCTGAAGGGCGGTACATTGC	1922
DB	2127	CC	GGGAGCAGCGGCACCCCGGCCGGCGGCACCTGCTGAAGGGCGGTACATTGC	2186
QY	1923	GG	GGCGCTGCCAGGCTCGCGAGCACTGATGAGCAACCGCTGCTCGAGGAGGAGGC	1982
DB	2187	GG	GGCGCTGCCAGGCTCGCGAGCACTGATGAGCAACCGCTGCTCGAGGAGGAGGC	2246
QY	1983	CG	CAGGAGGAGCAGCCACCTCTCGCCAAAGCCCTCATTTGAGACTGCCCTCG	2042
DB	2247	CG	CAGGAGGAGCAGCCACCTCTCGCCAAAGCCCTCATTTGAGACTGCCCTCG	2306
QY	2043	GC	TGCTCTGCGACCCACTTGTGACCGCTGGCCACAGCACTCCCTCGGAACATGACTC	2102
DB	2307	GC	TGCTCTGCGACCCACTTGTGACCGCTGGCCACAGCACTCCCTCGGAACATGACTC	2366
QY	2103	TC	GAGCACCCTCCCTCGAGGCTGCGGTGAGGCACAGCGACTCGCTCTCAGC	2162
DB	2367	TC	GAGCACCCTCCCTCGAGGCTGCGGTGAGGCACAGCGACTCGCTCTCAGC	2426
QY	2163	CC	CTCGGGGGCCCTATCAGGACATGGGCACTCCTCAGGCTCCACGAGCTCC	2222
DB	2427	CC	CTCGGGGGCCCTATCAGGACATGGGCACTCCTCAGGCTCCACGAGCTCC	2486
QY	2223	AT	CACTGTGGCCACCCAGGCACTCTCAGCAGAGGGCCATCCCGACAGCCCTTG	2282
DB	2487	AT	CACTGTGGCCACCCAGGCACTCTCAGCAGAGGGCCATCCCGACAGCCCTTG	2546
QY	2283	GG	GGCAGCAGCCCTTCTGCGCACCCCAAGCAGAGGTTCTGCCCCCAGAGGGCTGAG	2342
DB	2547	GG	GGCAGCAGCCCTTCTGCGCACCCCAAGCAGAGGTTCTGCCCCCAGAGGGCTGAG	2606
QY	2343	CC	CCCCACCCAGAGTTGCCCAATGCCCTCTGGCTCTTCTCCTCAGGATCTTGCAAGA	2402
DB	2607	CC	CCCCACCCAGAGTTGCCCAATGCCCTCTGGCTCTTCTCCTCAGGATCTTGCAAGA	2666
QY	2403	GG	CCCCCTTAGTACCTCAAGCCCTTCTTGGAACAGCCCGCAGGCAACCCCTCGCCCTGC	2462
DB	2667	GG	CCCCCTTAGTACCTCAAGCCCTTCTTGGAACAGCCCGCAGGCAACCCCTCGCCCTGC	2726
QY	2463	CAA	AGCAAGCCCCCAATTGGACTCTAAGATGGGGCTTGAGACATCTCTCTTCTCTGGAG	2522
DB	2727	CAA	AGCAAGCCCCCAATTGGACTCTAAGATGGGGCTTGAGACATCTCTCTTCTCTGGAG	2786
QY	2523	GC	CAAAACCCGGCCCTCGAGTTCCCGAGGCTCAGCTCCACAGGCGAGCTCTTCTCCCAAGT	2582

Db	2787	GCCTCTCAGTGCAGTCTGCGGCTTCCCAAGGTGAGCTTCCAGGCGAGCTCTTCCCAAGT	2846
Qy	2583	GAGTCTCCTCAGGTTGGCTCTCTCCCAAGTGGGCACAGAGCTTGCGCCCTCTCTGGATGC	2642
Db	2847	GAGTCTCCTCAGGTTGGCTCTCTCCCAAGTGGGCACAGAGCTTGCGCCCTCTCTGGATGC	2906
Qy	2643	GGAGGCTTGGACCCACAGAGGCTGAGGATCTGTCCGATCCACACCCACCTTGCAGGGCC	2702
Db	2907	GGAGGCTTGGACCCACAGAGGCTGAGGATCTGTCCGATCCACACCCACCTTGCAGGGCC	2966
Qy	2703	TCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTTCGCGGGGCTACGACGCGT	2762
Db	2967	TCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTTCGCGGGGCTACGACGCGT	3026
Qy	2763	GGCTGGCTATGGCACTTTGCTTTGTGTGAGATGACAGGGGCACTGCTGGGCGAGGGCC	2822
Db	3027	GGCTGGCTATGGCACTTTGCTTTGTGTGAGATGACAGGGGCACTGCTGGGCGAGGGCC	3086
Qy	2823	CATGTGGGCCAAGATAGCCTGGGTGTCTCCAGTCCGAGGAGGAGCAGGAGGAGGC	2882
Db	3087	CATGTGGGCCAAGATAGCCTGGGTGTCTCCAGTCCGAGGAGGAGCAGGAGGAGGC	3146
Qy	2883	CAGGGCTGAGTCCAGTCCGAGGAGCAGCAGGAGGCCAGGGCTTGAGAGGCCACTGCCCCA	2942
Db	3147	CAGGGCTGAGTCCAGTCCGAGGAGCAGCAGGAGGCCAGGGCTTGAGAGGCCACTGCCCCA	3206
Qy	2943	GGTCAGTGCAGAGGCTGTGCTGAGTTCGGCAGGGCTCCACACGAGGAGTCTCCAGAGCC	3002
Db	3207	GGTCAGTGCAGAGGCTGTGCTGAGTTCGGCAGGGCTCCACACGAGGAGTCTCCAGAGCC	3266
Qy	3003	CACCCCATGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCGGGAGCCTGTCAAGTGA	3062
Db	3267	CACCCCATGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCGGGAGCCTGTCAAGTGA	3326
Qy	3063	TGCGAGGGCGGCCGACCAATATATCCCTTGGACATTTCCGAGGTGGAACCCGCCCTACCTCAA	3122
Db	3327	TGCGAGGGCGGCCGACCAATATATCCCTTGGACATTTCCGAGGTGGAACCCGCCCTACCTCAA	3386
Qy	3123	CCTCTCAGACCTGTACCATATCAAGTACTCCCATTCAGTCTTTATGATCTTCAGGAAAGT	3182
Db	3387	CCTCTCAGACCTGTACCATATCAAGTACTCCCATTCAGTCTTTATGATCTTCAGGAAAGT	3446
Qy	3183	CCCCAAGTCCGCTCAGCAGAGCGCCCTCCGCCATGGCTGAGGAGAGCTGCCCGAGTT	3242
Db	3447	CCCCAAGTCCGCTCAGCAGAGCGCCCTCCGCCATGGCTGAGGAGAGCTGCCCGAGTT	3506
Qy	3243	CCCGAGGCCACGTCGGCCCTGGCCAGGTGAACCTGGGCCCCACGAGAGGCTCGAGATCAC	3302
Db	3507	CCCGAGGCCACGTCGGCCCTGGCCAGGTGAACCTGGGCCCCACGAGAGGCTCGAGATCAC	3566
Qy	3303	AGAGGATCAGAGATGTGGACGCGCTGTGGCAGAGGCTGCCGTGGCGAGGAGCGCAA	3362
Db	3567	AGAGGATCAGAGATGTGGACGCGCTGTGGCAGAGGCTGCCGTGGCGAGGAGCGCAA	3626
Qy	3363	GTGTCCTCCGCGTCAAGCAGCTCTTCCACTTCCCTGGGAGGCACTGCCGCTGGATGA	3422
Db	3627	GTGTCCTCCGCGTCAAGCAGCTCTTCCACTTCCCTGGGAGGCACTGCCGCTGGATGA	3686
Qy	3423	GCCTCAGAGCTGGGCTCGGTGAGAGGTGAAGGCTCCGTGGAGCAGATCTCCCGGAT	3482
Db	3687	GCCTCAGAGCTGGGCTCGGTGAGAGGTGAAGGCTCCGTGGAGCAGATCTCCCGGAT	3746
Qy	3483	CCTGAAGGCGAGGCCGGAAGGTCTGGAGAGGAGGGGCCCCCGCAGGAAGACCGAGCCT	3542
Db	3747	CCTGAAGGCGAGGCCGGAAGGTCTGGAGAGGAGGGGCCCCCGCAGGAAGACCGAGCCT	3806
Qy	3543	TGCTTCTCTCCGGCTCTCAGGCTTGAGAGCTGGGACCGAGCGCCACATCTCTAAGGA	3602
Db	3807	TGCTTCTCTCCGGCTCTCAGGCTTGAGAGCTGGGACCGAGCGCCACATCTCTAAGGA	3866
Qy	3603	GCTCTCAGATGAGACTGTGTCTTGGGCCAGTCAAGTGAATCTGGCTGCGAGGTGTACG	3662

DB	3867	GCTCTCAGATGAGACTGTGTGTTCTCTGGGCCCACTGTCAGTGCACATGCGCTGCCAGTGTGCAGC	3922
QY	3663	CCAGCCAGCTGCCCCAGGCGCACTGGAGCAAGAAGCGAGCCGCCCTCGTGAGACGACGAGCCG	3722
DB	3927	CCAGCCAGCTGCCCCAGGCGCACTGGAGCAAGAAGCGAGCCGCCCTCGTGAGACGACGAGCCG	3986
QY	3723	TGTCCTCATCTCTGCCACCTCTGAAGAACTTCAGCTTCAGCAATCCTGGTGGTGGTGGC	3782
DB	3987	TGTCTCTCATCTCTGCCACCTCTGAAGAACTTCAGCTTCAGCAATCCTGGTGGTGGTGGC	4046
QY	3783	TGAGGACCTGGGTGTGTACACCTTCGACGCGTGAACAATGGCTGGGACACAGTACCAACCAC	3842
DB	4047	TGAGGACCTGGGTGTGTACACCTTCGACGCGTGAACAATGGCTGGGACACAGTACCAACCAC	4106
QY	3843	GGGGCTCCTCGGAAGGACAGAGCGCCCTCATCTTCGCCATGCCCGGATATGGGGAGGT	3902
DB	4107	GGGGCTCCTCGGAAGGACAGAGCGCCCTCATCTTCGCCATGCCCGGATATGGGGAGGT	4166
QY	3903	GTACGCGGATGGGGTGTGTGTCTCTGGAAGCCCGTGGAAATCCTACGGCCCTGTGACCTTA	3962
DB	4167	GTACGCGGATGGGGTGTGTGTCTCTGGAAGCCCGTGGAAATCCTACGGCCCTGTGACCTTA	4226
QY	3963	CATTGTGCAGTCAGACCTAGAAGCGCGCAGCTGGACACACATGGCCCTCCGACATCTTGA	4022
DB	4227	CATTGTGCAGTCAGACCTAGAAGCGCGCAGCTGGACACACATGGCCCTCCGACATCTTGA	4286
QY	4023	CTGTGCTTACTGACCCAGCAAGCTCTCCGGGGTGGCACTTACACTTCGCAACGGCATG	4082
DB	4287	CTGTGCTTACTGACCCAGCAAGCTCTCCGGGGTGGCACTTACACTTCGCAACGGCATG	4346
QY	4083	TGTCAGCAAGCGAGGAATGGGTCCCTACAGACGCCCTCGGAGCAAGTCTCTCTGGAGG	4142
DB	4347	TGTCAGCAAGCGAGGAATGGGTCCCTACAGACGCCCTCGGAGCAAGTCTCTCTGGAGG	4406
QY	4143	GCCCGACCACTGGCTCTGAGAGAGAGACGAGGGGGGTGAGGCCAAACCCCTGCCCAAG	4202
DB	4407	GCCCGACCACTGGCTCTGAGAGAGAGACGAGGGGGGTGAGGCCAAACCCCTGCCCAAG	4466
QY	4203	CACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGGCCA	4262
DB	4467	CACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGGCCA	4526
QY	4263	ATGCTGGGAAGGCGCAGCGGGCGGGCGTGGCGGCCAAGATCATCCCTACACCCCA	4322
DB	4527	ATGCTGGGAAGGCGCAGCGGGCGGGCGTGGCGGCCAAGATCATCCCTACACCCCA	4586
QY	4323	GGACAAGACAGTGTCTGCGGAATACGAGGCCCTCAAGGGCCCTGCGCACCCGACCT	4382
DB	4587	GGACAAGACAGTGTCTGCGGAATACGAGGCCCTCAAGGGCCCTGCGCACCCGACCT	4646
QY	4383	GGCCAGCTGCACGACGCTACTGAGCCCGCGCACCTGGTGTCTATCTTGGAGCTGTG	4442
DB	4647	GGCCAGCTGCACGACGCTACTGAGCCCGCGCACCTGGTGTCTATCTTGGAGCTGTG	4706
QY	4443	CTCTGGGCCCGAGCTGCTCCCTGCTGGCCGAGAGGGCTCTTACTCAGAAATCTGAGGT	4502
DB	4707	CTCTGGGCCCGAGCTGCTCCCTGCTGGCCGAGAGGGCTCTTACTCAGAAATCTGAGGT	4766
QY	4503	GAGGACTACCTGTGGCAGATGTTGAGTGCACCCAGTACCTGCGACACACGACATCCT	4562
DB	4767	GAGGACTACCTGTGGCAGATGTTGAGTGCACCCAGTACCTGCGACACACGACATCCT	4826
QY	4563	GCACCTGGACCTGAGGTCCGAAACATGATCATCAACCGAATACAACCTGCTCAAGGTGCT	4622
DB	4827	GCACCTGGACCTGAGGTCCGAAACATGATCATCAACCGAATACAACCTGCTCAAGGTGCT	4886
QY	4623	GGACCTGGGCAATGCAACAGGCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAA	4682
DB	4887	GGACCTGGGCAATGCAACAGGCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAA	4946
QY	4683	GGACTACTAGAACCAATGGCTCCAGAGCTCTCTGAGAGGCCAGGGGGTGTTCACAGAC	4742
DB	4947	GGACTACTAGAACCAATGGCTCCAGAGCTCTCTGAGAGGCCAGGGGGTGTTCACAGAC	5006

Db	801	CTGTGTTGGTCATCTCTGCCGGGAGACATTAATAATCTCGGACTTTTGGCTTTGCCCGAGAA	860
QY	1038	CATCACCCAGCAGAGCTGCAGTTTCAGCCAGTACGGCTCCCCGTGAGTTGCTTCCCCCCGA	1097
Db	861	CATCACCCAGCAGAGCTGCAGTTTCAGCCAGTACGGCTCCCCGTGAGTTGCTTCCCCCCGA	920
QY	1098	GATCATCCAGCAGAAACCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTGATCTC	1157
Db	921	GATCATCCAGCAGAAACCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTGATCTC	980
QY	1158	CTACCTCAGCCTGACCTGTCTCATCCCCATTTGCCGCGAGAGTGACCGTGCACCCCTCT	1217
Db	981	CTACCTCAGCCTGACCTGTCTCATCCCCATTTGCCGCGAGAGTGACCGTGCACCCCTCT	1040
QY	1218	GAAAGTCTTGAGGGGGCGGTGTCTATGGAGCAGCCCCCATGGCTGCCACCTCAGCGAGA	1277
Db	1041	GAAAGTCTTGAGGGGGCGGTGTCTATGGAGCAGCCCCCATGGCTGCCACCTCAGCGAGA	1100
QY	1278	CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGGCTAGTGC	1337
Db	1101	CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGGCTAGTGC	1160
QY	1338	CCAGTGCCTCTCCCAACCCCTGGTTCTGTAAATCCATGCTCGGAGGAGCCCATTTCA	1397
Db	1161	CCAGTGCCTCTCCCAACCCCTGGTTCTGTAAATCCATGCTCGGAGGAGCCCATTTCA	1220
QY	1398	CACACCAAGCAGCTCAAGTTCTCTCGGCCGGAAGTTCGTGGCAGCGTTCCCTGATGAG	1457
Db	1221	CACACCAAGCAGCTCAAGTTCTCTCGGCCGGAAGTTCGTGGCAGCGTTCCCTGATGAG	1280
QY	1458	CTCAAGTCCATCCTGTGTATGCGCTCCATCTCCTGAGCTGTGCGGGGCCACCCGACAG	1517
Db	1281	CTCAAGTCCATCCTGTGTATGCGCTCCATCTCCTGAGCTGTGCGGGGCCACCCGACAG	1340
QY	1518	CCCTCTCCTCGGGTAGCCCGGCACCTCTGCAGGGACATGGTGGCTCTCCAGTTTCCTC	1577
Db	1341	CCCTCTCCTCGGGTAGCCCGGCACCTCTGCAGGGACATGGTGGCTCTCCAGTTTCCTC	1400
QY	1578	CTCCTCTCTGACAAACGAGCTCGCCCCCATTTGCCCGGGTAACTCACTGCACCCCTCCC	1637
Db	1401	CTCCTCTCTGACAAACGAGCTCGCCCCCATTTGCCCGGGTAACTCACTGCACCCCTCCC	1460
QY	1638	GGTGACACACTACCACTGTGTGACCCCGGGGCTTCCTCGGCCCTTCGGCAGCGTGGC	1697
Db	1461	GGTGACACACTACCACTGTGTGACCCCGGGGCTTCCTCGGCCCTTCGGCAGCGTGGC	1520
QY	1698	TGAGGAAGCGAGGCCATGAGCGCTCCACCGAGGGCCCCAGCTCCGCTGCATCTCCCGA	1757
Db	1521	TGAGGAAGCGAGGCCATGAGCGCTCCACCGAGGGCCCCAGCTCCGCTGCATCTCCCGA	1580
QY	1758	GGGTGCGGGCCACCGGCCCGCAGGGCTTCGTGTCCCGGACACAGCGTCACTCCGAGCCT	1817
Db	1581	GGGTGCGGGCCACCGGCCCGCAGGGCTTCGTGTCCCGGACACAGCGTCACTCCGAGCCT	1640
QY	1818	GTTCCTACCAACAGCGGGTGCAGACCTGTGAGCAGCGGGCCCTGGCCCGGGAGCAGGCG	1877
Db	1641	GTTCCTACCAACAGCGGGTGCAGACCTGTGAGCAGCGGGCCCTGGCCCGGGAGCAGGCG	1700
QY	1878	GCACCCGGCCCGGGCGGCACCTGTGTGAAGGGCGGCTACATTCGCGGGGCGTGTCCAGG	1937
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VERSION AX039412.1 GI:11229480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

AX039412 7928 bp DNA linear PAT 18-NOV-2000

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Zeng, W., Stanton, L. and Kong, H.
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SCIOS INC. (US)

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 94.4%; Score 4915.8; DB 6; Length 7928;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4920; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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VERSION AB046859.1 GI:10047354
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 4041)
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp).
URL: http://www.kazusa.or.jp/huge, Tel: 81-438-52-3913,
Fax: 81-438-52-3914

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ORIGIN

Query Match 77.2%; Score 4020.2; DB 9; Length 4041;
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Qy	1199	GTGACCGTGCACCCCTCTGAAACGTCTCTGGAGGGGCGGTGTGATGGAGCAGCCCATGG 1258
Db	61	GTGACCGTGCACCCCTCTGAAACGTCTCTGGAGGGGCGGTGTGATGGAGCAGCCCATGG 120
Qy	1259	CTGCCCACTCAGCGAAGACGCAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTC 1318
Db	121	CTGCCCACTCAGCGAAGACGCAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTC 180
Qy	1319	AGGCGCGGCTAGTGGCGGCGGAGTCTCTCCACCCCTGGTTCCTGAAATCCATGCTG 1378
Db	181	AGGCGCGGCTAGTGGCGGCGGAGTCTCTCCACCCCTGGTTCCTGAAATCCATGCTG 240
Qy	1379	CGGAGGAGCCACTTCATCAACACGACGAGCTCAAGTTCTCTGCGCCCGAAGTCGCT 1438
Db	241	CGGAGGAGCCACTTCATCAACACGACGAGCTCAAGTTCTCTGCGCCCGAAGTCGCT 300
Qy	1439	GGCAGCGTTCCCTGATGAGCTACAAGTCCATCTCTGGTGTGCGCTCCATCCCTGAGCTGC 1498
Db	301	GGCAGCGTTCCCTGATGAGCTACAAGTCCATCTCTGGTGTGCGCTCCATCCCTGAGCTGC 360
Qy	1499	TGCGGGGCGCCACCGACAGCCCTCTCTCGGCGTAGCCCGGACCTCTGACGAGCACTG 1558
Db	361	TGCGGGGCGCCACCGACAGCCCTCTCTCGGCGTAGCCCGGACCTCTCTGACGAGCACTG 420
Qy	1559	GTGGCTCTCCGATTCCTCTCTCTGTGACAAAGAGCTCGGCCCATTTGGCGGGGCTA 1618
Db	421	GTGGCTCTCCGATTCCTCTCTCTGTGACAAAGAGCTCGGCCCATTTGGCGGGGCTA 480
Qy	1619	AGTCACTGCCACCTCCCGGTGACACACTCACCAGCTGTGACCCCGGGGCTTCTGTC 1678
Db	481	AGTCACTGCCACCTCCCGGTGACACACTCACCAGCTGTGACCCCGGGGCTTCTGTC 540
Qy	1679	GGCCCTCGGCGAGCTGTCTGAGAGGCGGAGGCGCTGAGCGCTCCACCGAGGCCCGAG 1738
Db	541	GGCCCTCGGCGAGCTGTCTGAGAGGCGGAGGCGCTGAGCGCTCCACCGAGGCCCGAG 600
Qy	1739	CTCCGCTGCACTCTCCGAGGGTCCGGGCGACCGGCGGCGGAGGCTGCTGCCCGGC 1798
Db	601	CTCCGCTGCACTCTCCGAGGGTCCGGGCGACCGGCGGCGGAGGCTGCTGCCCGGC 660
Qy	1799	ACAGCGTCACTCGCAGCGCTTCTTACCAACGAGGCGGTGAGAGCCCTGAGCAGGGGCGC 1858
Db	661	ACAGCGTCACTCGCAGCGCTTCTTACCAACGAGGCGGTGAGAGCCCTGAGCAGGGGCGC 720
Qy	1859	TGGCGCGGGGAGCAGGCGGCAACCGGCGGCGGCGGCACTTGTGAGGGCGGTACA 1918
Db	721	TGGCGCGGGGAGCAGGCGGCAACCGGCGGCGGCGGCACTTGTGAGGGCGGTACA 780
Qy	1919	TTGGCGGGGCGCTGCGAGGCTGCGGAGCGCACTGTATGGAGCACCGGCTGCTGGAGAG 1978
Db	781	TTGGCGGGGCGCTGCGAGGCTGCGGAGCGCACTGTATGGAGCACCGGCTGCTGGAGAG 840
Qy	1979	AGGCGCGCAGGAGGAGCAGCGCACTCTCTGGCGAAGCGCCCTCATTCGAGACTGCC 2038
Db	841	AGGCGCGCAGGAGGAGCAGCGCACTCTCTGGCGAAGCGCCCTCATTCGAGACTGCC 900
Qy	2039	TCCGGCTGCTCTCTGGCAACCACTTGGCCCTTGGCCACAGCCACTCTCTGGAAATG 2098
Db	901	TCCGGCTGCTCTCTGGCAACCACTTGGCCCTTGGCCACAGCCACTCTCTGGAAATG 960
Qy	2099	ACTCTCCGAGCACCCCGCCCTCTCTCGGAGGCGCTCGGGTGGAGGACAGCGACTGCTT 2158

Db	961	ACTCTCCGAGCACCCCGCCCTCTCTCGAGGCGCTCGGGTGGGACAGCGACTGCTT 1020
Qy	2159	CAGCCCCCTCCGGGGGGGCCCTTATCAGGAGCATATGGGACACCTCTCAGGGTCCCAAGCAGC 2218
Db	1021	CAGCCCCCTCCGGGGGGGCCCTTATCAGGAGCATATGGGACACCTCTCAGGGTCCCAAGCAGC 1080
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Db	1081	TTCCATCCACTGTGTGGCCACCCAGGCACTGCTCAGCCAGAGAGCCATCCCGGACAGC 1140
Qy	2279	CTTGGGGGCGAGCAGCCCTTTCTGCGACCCCAAGCAGAGGTTCTGCCCCCGCAGAGGGCT 2338
Db	1141	CTTGGGGGCGAGCAGCCCTTTCTGCGACCCCAAGCAGAGGTTCTGCCCCCGCAGAGGGCT 1200
Qy	2339	GCAGCCCCCAGCAGAGTTGCCCCATGCCCCCTCTCTGGCTCTCTCCCTCAGAGTCTTGA 2398
Db	1201	GCAGCCCCCAGCAGAGTTGCCCCATGCCCCCTCTCTGGCTCTCTCCCTCAGAGTCTTGA 1260
Qy	2399	AAGAGGGCCCTTAGTACCTTCAAGCCCTTCTTGGGACAGCCCGCAGGACCCCTTGC 2458
Db	1261	AAGAGGGCCCTTAGTACCTTCAAGCCCTTCTTGGGACAGCCCGCAGGACCCCTTGC 1320
Qy	2459	CTGCCAAGCAAGCCCCCCTAGTGAATAGATGGGCTGGAGACATCTCTTCTCTG 2518
Db	1321	CTGCCAAGCAAGCCCCCCTAGTGAATAGATGGGCTGGAGACATCTCTTCTCTG 1380
Qy	2519	GGAGGCAAAACCCGGCCCTGCACTTCCCAAGGTCAGCCTCCCAAGGCGAGCTTCC 2578
Db	1381	GGAGGCAAAACCCGGCCCTGCACTTCCCAAGGTCAGCCTCCCAAGGCGAGCTTCC 1440
Qy	2579	AAGTGAGCTCCCTCAGGTTGGGCTCTCCAGGTGGGACAGAGCTGGCCCTCCCTG 2638
Db	1441	AAGTGAGCTCCCTCAGGTTGGGCTCTCTCCAGGTGGGACAGAGCTGGCCCTCCCTG 1500
Qy	2639	ATGCGGAGGCTGGACCCAGGAGCTGAGGATCTGTCGACTCCACCCACTTTCAGC 2698
Db	1501	ATGCGGAGGCTGGACCCAGGAGCTGAGGATCTGTCGACTCCACCCACTTTCAGC 1560
Qy	2699	GGCTCAGGAAACAGGTGACCATGCGCAAGTTCTCCCTGGTGGTGGCGGGCTACGAG 2758
Db	1561	GGCTCAGGAAACAGGTGACCATGCGCAAGTTCTCCCTGGTGGTGGCGGGCTACGAG 1620
Qy	2759	GCCTGGCTATGGCACTTTGCTTTGGTGGAGATCAGGGGGCATGTGGGGCAGG 2818
Db	1621	GCCTGGCTATGGCACTTTGCTTTGGTGGAGATCAGGGGGCATGTGGGGCAGG 1680
Qy	2819	GGCCCATGTGGGCGAGGATAGCTGGCTGTGTCAGTCGAGGAGGAGGAGGAGGAGG 2878
Db	1681	GGCCCATGTGGGCGAGGATAGCTGGCTGTGTCAGTCGAGGAGGAGGAGGAGGAGG 1740
Qy	2879	AGCCAGGCTGAGTCCAGTCCGAGGAGCAGCAGAGGCGCAGGCTGAGAGCCACTGC 2938
Db	1741	AGCCAGGCTGAGTCCAGTCCGAGGAGCAGCAGAGGCGCAGGCTGAGAGCCACTGC 1800
Qy	2939	CCAGGTCAGTCAAGGCTGTGCTGAGTGGGAGGCTCCCAAGGAGCTCTCCAG 2998
Db	1801	CCAGGTCAGTCAAGGCTGTGCTGAGTGGGAGGCTCCCAAGGAGCTCTCCAG 1860
Qy	2999	AGGCCACCCCATGGGAGGACATCGGCGAGTCTCCCTGTGTCAGATCCGGGACCTGT 3058
Db	1861	AGGCCACCCCATGGGAGGACATCGGCGAGTCTCCCTGTGTCAGATCCGGGACCTGT 1920
Qy	3059	GTGATGGGAGGCGCGCACAAATATCCCTGACATTTCCGAGGTGGACCCCGCTACC 3118
Db	1921	GTGATGGGAGGCGCGCACAAATATCCCTGACATTTCCGAGGTGGACCCCGCTACC 1980
Qy	3119	TCAACCTCTCAGACCTGTACGATATCAAGTACTCTCCCATTCAGTTTATGATCTTCAGGA 3178
Db	1981	TCAACCTCTCAGACCTGTACGATATCAAGTACTCTCCCATTCAGTTTATGATCTTCAGGA 2040
Qy	3179	AAGTCCCAAGTCCGCTCAGCGAGGCGCCCTTCCCCATGCTGAGGAGGAGCTGGCG 3238

QY	3838	ACCACGGGCGTCTCTCGGAAGGCAGAGCGCCCTCATCTTCGCCATGCCGGATATCGGG	3897
Db	1873	ACCA CGGCGTCTCTCGGAAGGCAGAGCGCCCTCATCTTCGCCATGCCGGATATCGGG	1932
QY	3898	GAGGTGTACGGGATGGGGTGTCTGGTCTGGAAGCCCGTGGAACTCTACGGCCCTGTG	3957
Db	1933	GAGGTGTACGGGATGGGGTGTCTGGTCTGGAAGCCCGTGGAACTCTACGGCCCTGTG	1992
QY	3958	ACCTACATTTGTGCAGTGCAGCCTTAGAAGCGGCAGCTGGACACACACTGGCCCTCGACATC	4017
Db	1993	ACCTACATTTGTGCAGTGCAGCCTTAGAAGCGGCAGCTGGACACACACTGGCCCTCGACATC	2052
QY	4018	TTTGA CTGCTGTACCTGAC CAGCAAGCTCTCCGGGGTGGCACCTACACCTTCGGCAG	4077
Db	2053	TTTGA CTGCTGTACCTGAC CAGCAAGCTCTCCGGGGTGGCACCTACACCTTCGGCAG	2112
QY	4078	GCATGTGT CAGCAAGCAGGAATGGGTCCCTACAGCAGCCCTTCGAGCAAGTCTCTCTG	4137
Db	2113	GCATGTGT CAGCAAGCAGGAATGGGTCCCTACAGCAGCCCTTCGAGCAAGTCTCTCTG	2172
QY	4138	GGAGGCCACAGCCACTGTGGCTCTGAGAGGAGAGCCAGGGGGCGTTCAGCCCAACCCCTG	4197
Db	2173	GGAGGCCACAGCCACTGTGGCTCTGAGAGGAGAGCCAGGGGGCGTTCAGCCCAACCCCTG	2232
QY	4198	CCAGCAGCAAGACCTTTCGATTTCCAGACACAGATCCAGAGGGGGCGCTTCAGCGTGGTG	4257
Db	2233	CCAGCAGCAAGACCTTTCGATTTCCAGACACAGATCCAGAGGGGGCGCTTCAGCGTGGTG	2292
QY	4258	CGGCAATGCTGGGAGAAAGCCAGCGGGCGGGCGCTGGCCGCCAAGATCATCCCTTACCAC	4317
Db	2293	CGGCAATGCTGGGAGAAAGCCAGCGGGCGGGCGCTGGCCGCCAAGATCATCCCTTACCAC	2352
QY	4318	CCCAAGGACAAGACAGCAGTGTCTCGCGAATAGAGGCCCTCAAGGGCCTGCGCCACCCG	4377
Db	2353	CCCAAGGACAAGACAGCAGTGTCTCGCGAATAGAGGCCCTCAAGGGCCTGCGCCACCCG	2412
QY	4378	CACCTGGCC CAGCTGCACGAGCCTTACTCAGCCCCCGGCACCTGTGTCTATCTTTGGAG	4437
Db	2413	CACCTGGCC CAGCTGCACGAGCCTTACTCAGCCCCCGGCACCTGTGTCTATCTTTGGAG	2472
QY	4438	CTGTGCTCTGGGGCCGAGCTGTCTCCCTGCTGGCCGAGAGGGCCTCCTACTCAGAATCT	4497
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QY	4498	GAGGTGAAGGACTACTGTGTGGCAGATGTTGAGTGCACCCAGTACCTGCACACACGAC	4557
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QY	4558	ATCTGTGACCTGTGACCTGAGGTCCGAGAAATGATCATCACCGAATCAACCTGCTCAAG	4617
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QY	4618	GTCTGTGACCTGGGCAATGCA CAGAGCCTCAGCCAGGAGAGGTGTCTCCCTCAGACAAG	4677
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QY	4738	CAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCTGCTGAGGGCCGAGTACCG	4797
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QY	4798	GTGACACGAGGGGTGCACGGCACTCTGCAGAGAGGACTGCGCAAGGGGCTGGTCCGGCTG	4857
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QY	4858	AGCCGCTGCTACCGGGGCTGTCCGGGGCGCGCTGGCTTCCTGCGCAGACACTCTGTC	4917
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FEATURES

Qy	4918	GCCACGCCCTGGGGCGGGCCTGCGGGTCCAGCTGCAGTGCCTGCGGCTAACACAG	4977
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Qy	4978	GAGGCGCCGCGCCTGTTTCGCGGGCCGCGCCCGTGAACCTCCCTACCGCGCGGCTGCGCGTC	5037
Db	3013	GAGGCGCCGCGCCTGTTTCGCGGGCCGCGCCCGTGAACCTCCCTACCGCGCGGCTGCGCGTC	3072
Qy	5038	TTTCGTGGCAATCGCGCAGAGAGACGCGGGCTGCTGTACAAGAGGCACAACTGCGCCACG	5097
Db	3073	TTTCGTGGCAATCGCGCAGAGAGACGCGGGCTGCTGTACAAGAGGCACAACTGCGCCACG	3132
Qy	5098	GTGCGGTGAGGGTCGCGCGGCCACACCTTGGTCTCCCGGCTGGGGGTTCGCTGCAGACG	5157
Db	3133	GTGCGGTGAGGGTCGCGCGGCCACACCTTGGTCTCCCGGCTGGGGGTTCGCTGCAGACG	3192
Qy	5158	CGCCAAATAAAAAACGCACAGCGCGGGCGAGAAAA	5190
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RESULT 11

AL670729

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human DNA sequence from clone RP11-245P10 on chromosome 1, complete sequence.

AL670729.19 GI:22316158

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 62164)

Van Hellmond, Z.

Direct Submission

Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 15, 2002 this sequence version replaced gi:21727388.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/c_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> <http://www.sanger.ac.uk/HGP/Chr1> RPL1-245P10 is from the library RPL1-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> vector: pBACe3.6.


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Db      26339  CCTGGAGGACCTCCCTGGATGAGCTCAGAGCTGGGCTGGCTGAGAGTGAAG 26398
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RESULT 12
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LOCUS Homo sapiens chromosome 1 clone RP11-661B12, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.
ACCESSION AC023889
VERSION AC023889.3 GI:8969253
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 174612)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 174612)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jul 7, 2000 this sequence version replaced gi:8748947.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH061B12
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator; 100% of reads
Assembly: Dye-terminator Big Dye; 0% of reads
Consensus quality: 163945 bases at least Q40
Consensus quality: 167601 bases at least Q30
Consensus quality: 169687 bases at least Q20
Insert size: 148000; agarose-fp
Insert size: 173412; sum-of-contigs
Quality coverage: 5.67 in Q20 bases; agarose-fp
Quality coverage: 5.55 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2478: contig of 2478 bp in length
* 2479 2578: gap of unknown length
* 2579 5948: contig of 4370 bp in length
* 5949 7048: gap of unknown length
* 7049 9374: contig of 2325 bp in length
* 9374 9473: gap of unknown length
* 9474 13303: contig of 3830 bp in length
* 13304 13403: gap of unknown length
* 13404 18271: contig of 4867 bp in length
* 18271 18371: gap of unknown length
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* 25698 34815: contig of 9126 bp in length

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* 34816 34915: gap of unknown length
* 34916 45742: contig of 10827 bp in length
* 45743 45842: gap of unknown length
* 45843 62987: contig of 17145 bp in length
* 62988 63087: gap of unknown length
* 63088 87584: contig of 24497 bp in length
* 87585 87685: gap of unknown length
* 87686 114765: contig of 27081 bp in length
* 114766 114865: gap of unknown length
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Best Local Similarity 97.2%; Pred. No. 2.3e-221;
Matches 1641; Conservative 0; Mismatches 35; Indels 13; Gaps 9;

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Qy      1876  CGGCACCGCGCGCGCGGCACCTGCTGGAAGGGCGGTACATTCGGGGCGCGCTGCCA 1935
Db      25345  CGAAACCGCG--GCACAGTCGGCACCTGCTGAAGGGCGGTACATTGCGGG--GCTGCCA 25289
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Db      25288  GCGCTGGCGGAGCCACTGATGGAGAGCAGCGTGTGAGGAGGAGCGCCGAGGAGGAG 25229
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Db      25228  CAGGCACCCCTCTTGGCCAAAGCCCTCATTTGAGACTGCCCCCTCGCGTGTGCTCT 25169
Qy      2056  GGCACCCCACTTGGCCCTGGCCACAGCACTCCCTGGACATGACATCTCCGAGCACCCC 2115
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QY	2116	CGCCCTCTCTCGAGGCGCTGCGGTGAGGCA	CHAGCAGCTGCCTTCAGCCCCCTCGGGGG	2175
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QY	2176	GCCCCATCAGGCAATGGGGCACCTCAGGGCT	CCAAAGCAGCTTCATCCACATGSGTGGC	2235
Db	25052	CCCCCTATCAGGCAATGGGGCA-CTCAGGGCT	CCAGCAGCTTCATCCACATGSGTGGC	24994
QY	2236	CACCCAGGCACTGCTCAGCCAGAGAGGCAAT	CCCCCGACAGCCCTTGGGGGAGCCACGCC	2295
Db	24993	CACCCAGGCACTGCTCAGCCAGAGAGGCAAT	CCCCCGAGCAGCCCTTGGGGGAGCCACGCC	24934
QY	2296	CGTTTCTGCAACCCCAAGCAGAGGTTCTG	CCCCCGCCAGGAGGGCTGAGCGCCCCACCCAGCA	2355
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QY	2356	GTTGCCCAATGCCCTCTCGCTCTTCCCTCAG	AGATCTTGCAAGAGGCCCCCTTAGTA	2415
Db	24875	GTTGTTCCATGCCCTCTCGCTCTTCCCTCAG	AGATCTTGCAAGAGGAGCCCTTAGTA	24816
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QY	2596	GTGGGCTCTCCAGAGTGGGCAAGAGCC	TGGCCCTCCCTGGATGCGAGGGCTGGACC	2655
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Db	24396	ATAGCTGGGCTGTGTCACAGTCGGAG	GAGGAGCAGGAGCCAGGGCTCAGTGCC	24337
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Db	24336	CAGTCGGAGGAGCAGCAGGAGGCGCAG	GGGCTGAGAGCCACTGCCCAAGTCAGTGCAAGG	24277
QY	2956	CCTGTGCTCAGGTGCGCAGGGCTCCCA	CCAGAGGCTCTCCAGAGCCACCCCATGGGAG	3015
Db	24276	CCTGTGCTCAGGTGCGCAGGGCTCCCA	CCAGAGGCTCTCCAGAGCCACCCCATGGGAG	24217
QY	3016	GACATCGGCAGGTCCTCCCTGTGCGAT	CCGGGACCTGTCAAGTTCATCGGAGCGGCC	3075
Db	24216	GACATCGGCAGGTCCTCCCTGTGCGAT	CCGGGACCTGTCAAGTTCATCGGAGCGGCC	24157
QY	3076	GACACAATATCCCTTGGACAATTCGAG	GGTGGGACCCCGCCTTCAACTCTTCAGACCTG	3135
Db	24156	GACACAATATCCCTTGGACAATTCGAG	GGTGGGACCCCGCCTTCAACTCTTCAGACCTG	24097
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LOCUS					
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	SEQUENCE, 31 unordered pieces.				
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VERSION	AC026657.4	GI:9958202			
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ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 164766)				
AUTHORS	Waterston,R.H.				
TITLE	The sequence of Homo sapiens clone				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 164766)				
AUTHORS	Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-WAR-2000) Genome Sequencing Center, Washington				
	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
	MO 63108, USA				
COMMENT	On Sep 1, 2000 this sequence version replaced gi:7637349.				

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0245P10
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator; plasmid; 0%
Chemistry: Dye-terminator; Big Dye; 0% of reads
Assembly: Dye-terminator; Phrap; version 0.990319
Consensus quality: 139884 bases at least Q40
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Insert size: 169000; agarose-fp
Insert size: 161074; sum-of-contigs
Quality coverage: 3.60 in Q20 bases; agarose-fp
Quality coverage: 3.92 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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Mouse DNA sequence from clone RP23-44118 on chromosome 11, complete sequence.

AL662809

AL662809.14 GI:28881816

HTG

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 103129)

Direct Submission

Submitted (06-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk

HumQuery@sanger.ac.uk

On Mar 7, 2003 this sequence version replaced gi:21655347.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above, as we submit sequences with the following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
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 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 258622)
 DOE Joint Genome Institute.
 Direct Submission
 Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Mar 29, 2000 this sequence version replaced gi:5686431.
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 Center: Joint Genome Institute
 Web site: <http://www.jgi.doe.gov>
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 Consensus quality: 208421 bases at least Q20
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 Estimated coverage: 4.19x in Q20 bases; pulse field gel estimation
 Quality coverage: 3.50x in Q20 bases; sum-of-contigs estimation

NOTE: This is a 'working draft' sequence. It currently

consists of 97 contigs. The true order of the pieces
 is not known and their order in this sequence record is
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 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
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 57171: contig of 1077 bp in length
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 58192: contig of 1021 bp in length
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 59434: contig of 1242 bp in length
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 62130: contig of 1482 bp in length
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 65248: contig of 1972 bp in length
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 67624: contig of 2376 bp in length
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* 76852 78211: contig of 1360 bp in length
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* 102978 106226: contig of 3249 bp in length
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* 107978 110243: contig of 2266 bp in length
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* 118029 120548: contig of 2520 bp in length
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Best Local Similarity 67.6%; Pred. No. 3e-117;
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QY 1458 CTACAAGTCCATCTGTGTATGCGCTCCATCCCTGAGCTGTGCGGGGCCCAACCGACAG 1517
DB 250154 CTACAAGTCTATCTGTGTATGCGCTCCATCCCTGAGCTGTGCTCAGGGTCCCGACAG 250095
QY 1518 CCCCTCCCTCGGGTAGCCCGGACCTCTGCGAGGACACTGGTGGCTCTCTCAGTTTCCTC 1577
DB 250094 TCCATCTTAGGAGTGGCCCGGCACTACAGGGGAAGCCAGTGGCGCTCTAGTCAATC 250035
QY 1578 CTCCTCTCTGACACAGGCTGCGCCCATTTGCGGGGTAGTCACTGCCACCTCCCTCCC 1637
DB 250034 ATCTCTCTGACACAGGCTTCCCATTTGCGAGGGTCAAGTGGCTGCCACCTCTCC 249975
QY 1638 GGTGACACATCACTGCTGACACCCCGGGGCTTCTGCGGCGCTCGGCCAGCTGCC 1697
DB 249974 TGTGACTCACTGCGCACTGTGCACTCGGGCTTCTGCGGCTTTCGGCCAGCTCC 249915
QY 1698 TGAGGAGCGGCGAGTGAAGCTCCACCGAGGCGGCTCCGCTGCTGATCTCCGA 1757
DB 249914 AGAGGAGACAGGCGCAGCATGCCACTGCTGATGCGGCG---TCCAGCGTCCCCACA 249858

QY 1758 GGGTGC CGGGCCACCGGCGCCGCCAGGGCTGCTGCCCGGCACAGCGTCTATCCGACGCT 1817
DB 249857 GAGTGTGCGGCTCCGGCAAGCCCGCAGGTTGTGTGCCCGGCACAGCTCATCAGACGCT 249798
QY 1818 GTTCTACACACAGCGGGTGAAGCCCTGAGCA GGGGCGCTGCTGGCGGGAGCAGCG 1877
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DB 249677 TCTGCGTGAAGCCCTCATGTGAGTACAGCTTGTGGAGGAAGAGCGGCTAGGGAAGCA 249618
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DB 249617 GGCCTCTCTGATGACCAAGACACCTCTTTGAGACTGCTGCTGCTGCTGCTGCTG 249558
QY 2058 CACCCACTTGGCCCTGGCCACAGCCACTCCTCGGAACATGACTCTCCGAGCAGCCCGCG 2117
DB 249557 TGTGAGAGAGTCCCGAGCGCGAGCCACTCCCTG---ACAAACCACAGTCAAGCTG 249501
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DB 249500 CCGCTCTCTGAGGCAATGAAGGAACACTCTCTTCCACCTCCACGGGTTGACTCA 249441
QY 2172 GGGGCGCCCTTATCAGGGACATGGGGCACCTCTCAGGGCTCCAAGCAG---CT 2219
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QY 2220 TCCATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGCCATCCCGGACAGCCC 2279
DB 249380 TCCACTATGATGTGTGACTCGAGGCTGGAGCAAGAGGATCATCCAGGACAGTTG 249321
QY 2280 TTGGGGGAGCGAGCCCTTTCTGCCACCCCAAGAGGTTTGTGCCCGCCAGAGGCGCTG 2339
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DB 249209 GAAGGAGCTCTCAACGTCCTGTGGCCCACTCTTTTCAGAACAGCCTCAGGACGCCCAT 249150
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DB 249149 CCAACTCAAGTAAGCCCTTCTGGGTTCTGAGAGGAACCTCAGGATGGCTCTCTATC 249090
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DB 249089 TGAAGGCCAGTTCCAGTTCCTCCAGTTCTCCAGGGTCAAGTCTTCCAAAGTA----- 249038
QY 2577 CCAAGTGAAGTCCCTCAGGGTGGGCTCTCTCCAGGTGGGCAACAGAGCTTGGCCCTCCCT 2636
DB 249037 -----GATGATCTCT 249027
QY 2637 GATGCGAGGCTGGACCCAGGAGGCTGAGGATCTGTCGAGCTCCACACCCACCTTGCA 2696
DB 249026 GATACTGAAGCTTGTG---TGAAGCTGGGACACATGTGACTTCACGCTCTCTCCACA 248970
QY 2697 GCGGCTCAGGAACAGGTGACCATGCGCAAGTTCTCTCTGGGTGGTCTCGGGGGCTTACGC 2756
DB 248969 GCGGCTCAGGAGCAGGCCACCCCGAAGTTCTCTCTGGAGTCCCGTGGGGGCTTATGC 248910
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Job time : 13046 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 12:45:44 ; Search time 1365 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues
Total number of hits satisfying chosen parameters: 5915158

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5207	100.0	5207	13	US-10-697-263-1
3	5207	100.0	5207	13	US-10-697-263-3
4	5173.6	99.4	5454	13	US-10-415-011-44
5	4940.4	94.9	8106	14	US-10-077-130-1
6	4940.4	94.9	24120	14	US-10-077-130-4
7	4915.8	94.4	5007	15	US-10-307-019-3
8	4915.8	94.4	7928	15	US-10-307-019-5
9	4885.2	93.8	4936	13	US-10-182-243-14
10	4841	93.0	7893	14	US-10-077-130-3
11	4841	93.0	23907	14	US-10-077-130-6
12	4146.6	79.6	4175	15	US-10-307-019-2
13	3197.8	61.4	3225	17	US-10-311-034-46
14	1251.4	24.0	1253	13	US-10-425-114-26278

ALIGNMENTS

RESULT 1
US-09-858-664A-1
; Sequence 1, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-858-664A-1

Query Match		100.0%;	Score 5207;	DB 9;	Length 5207;
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Db	1	CAGCAGAGAACTCTCTGATCAGCTGGCCAGCTGAGTTCAGAGTGGAGGAGGAGTGG	60		
Qy	61	GTTCATTGAAGAGTACTCTTAACCTGTGAGAGGCTGGCGGTGAGGATGGGGTGTGT	120		
Db	61	GTTCATTGAAGAGTACTCTTAACCTGTGAGAGGCTGGCGGTGAGGATGGGGTGTGT	120		
Qy	121	CGCTTGGCTGCGGGGGGTTCAGTTGGCCAGTGTATCTCAGGGTCTACCAACCAT	180		
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15	358.4	6.9	382	11	US-09-864-408A-8947	Sequence 8947, Ap
16	327.6	6.3	7789	13	US-10-333-314-38	Sequence 38, Appl
17	327.6	6.3	9698	16	US-10-210-130-37	Sequence 37, Appl
18	327.6	6.3	9807	16	US-10-379-381-1	Sequence 1, Appl
19	308.4	5.9	9930	16	US-10-210-130-33	Sequence 33, Appl
20	308.4	5.9	10122	16	US-10-210-130-35	Sequence 35, Appl
21	224.4	4.3	1627	13	US-10-425-114-26265	Sequence 26265, A
22	223.4	4.3	225	11	US-09-864-408A-2403	Sequence 2403, A
23	205.2	3.9	860	16	US-10-210-130-39	Sequence 39, Appl
24	173.4	3.3	2132	16	US-10-262-445-118	Sequence 118, Appl
25	173.4	3.3	2224	15	US-10-059-585-11	Sequence 11, Appl
26	157.2	3.0	1971	10	US-09-849-138-3	Sequence 3, Appl
27	157.2	3.0	2558	10	US-09-849-138-5	Sequence 5, Appl
28	153.8	3.0	1788	9	US-09-797-039-9	Sequence 9, Appl
29	153.8	3.0	1788	15	US-10-170-789-9	Sequence 9, Appl
30	153.8	3.0	1791	13	US-10-423-543-26	Sequence 26, Appl
31	153.8	3.0	2046	9	US-09-797-039-7	Sequence 7, Appl
32	153.8	3.0	2046	13	US-10-423-543-24	Sequence 24, Appl
33	153.8	3.0	2046	13	US-10-170-789-7	Sequence 7, Appl
34	153.8	3.0	3199	13	US-10-112-944-49	Sequence 49, Appl
35	153.6	2.9	8906	13	US-10-182-936A-85	Sequence 85, Appl
36	153.6	2.9	8906	16	US-10-374-979-85	Sequence 85, Appl
37	153.6	2.9	8906	16	US-10-331-498A-87	Sequence 87, Appl
38	152.2	2.9	1839	10	US-09-849-138-7	Sequence 7, Appl
39	152	2.9	3731	9	US-09-925-299-114	Sequence 114, App
40	148.6	2.9	3731	10	US-09-925-299-114	Sequence 114, App
41	148.6	2.9	1467	13	US-10-425-114-16427	Sequence 16427, A
42	148.6	2.9	3164	15	US-10-210-120-25	Sequence 25, Appl
43	148.6	2.9	4564	10	US-09-814-353-21660	Sequence 21660, A
44	148.6	2.9	5926	9	US-09-969-708-302	Sequence 302, App
45	148.6	2.9	5926	9	US-09-354-456-522	Sequence 522, App

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QY	361	GTGACCTGGTACAAGGACAGCGT	GCAGCTGTGGACAGCACCCGCTTAGCCACAGCAA	420
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QY	421	GAAGGCACACATCTCCCTGTGTG	TGAGGCAATGGGCTCGAAGATGCGCGTTTAC	480
Db	421	GAAGGCACACATCTCCCTGTGTG	TGAGGCAATGGGCTCGAAGATGCGCGTTTAC	480
QY	481	ACCTGGCTGGCCCAAACTGGTGG	CCAGAGTCTCGAAGGACAGAGCTGCTGGTGTT	540
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QY	541	GGGGGGGACAATGAGCCGACTCAG	AGAGCAAAAGCCACCGGAGGAAGCTGCATCTTC	600
Db	541	GGGGGGGACAATGAGCCGACTCAG	AGAGCAAAAGCCACCGGAGGAAGCTGCATCTTC	600
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QY	661	AAAGGAAAACAAGATCTGTGCGT	GCAGAGTTCATCCCTACGGAGCAGAACTCGGCCC	720
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QY	721	CAGGCATACAGGAGCGAGACAT	CTGTGGCGGCTGAGCCACCCGCTGTGCTGAGGCTG	780
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QY	781	CTGACCGATTGAGACCCGACAG	ACCTCATCTCTCATCTGAGCTGTGCTCATCCGAG	840
Db	781	CTGACCGATTGAGACCCGACAG	ACCTCATCTCTCATCTGAGCTGTGCTCATCCGAG	840
QY	841	GAGCTGTGACCGCTGTACAGAA	GGCGTGGTGAACGAGGCGAGGTCGAGTCAAGTCTAC	900
Db	841	GAGCTGTGACCGCTGTACAGAA	GGCGTGGTGAACGAGGCGAGGTCGAGTCAAGTCTAC	900
QY	901	ATCCAGAGCTGTGGAGGGCTGCA	CTACCTGCACAGCATGCGCTTCTCCACCTGGAC	960
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QY	1081	GAGTTCTCTCCCCGAGATCATCC	AGAGAACCTGTGAGCGAAGCCTCCGACATTTGG	1140
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QY	1201	GACCGTGCACCTCTCTGAGAGG	GGCGGTGTGTCATGGAGCAGACCCCATGGCT	1260
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QY	1321	GCCCGGCTAGTGGCGGCCAGTG	CCCTCTCCACCCCTGGTTCCTGAAATCCATGCGTGG	1380
Db	1321	GCCCGGCTAGTGGCGGCCAGTG	CCCTCTCCACCCCTGGTTCCTGAAATCCATGCGTGG	1380
QY	1381	GAGGAGGCCACTTCATCAACAC	CAAGAGCTCAAGTTCTCTCTGGCCCCGAAAGTCCGTGG	1440
Db	1381	GAGGAGGCCACTTCATCAACAC	CAAGAGCTCAAGTTCTCTCTGGCCCCGAAAGTCCGTGG	1440
QY	1441	CAGCGTTCCCTGATGAGCTACA	AGTTCATCTGTGTGATGGTCCATCTCTCTGAGTGTGG	1500
Db	1441	CAGCGTTCCCTGATGAGCTACA	AGTTCATCTGTGTGATGGTCCATCTCTCTGAGTGTGG	1500
QY	1501	CGGGGCCCCACCGACAGCCCT	CTCCCTCGGCTAGCCCGGACCTCTGCAAGGACACTGTGT	1560
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QY	1561	GGTCTCTCAGATTCTCTCTCT	CTGACAAACGAGCTCGCCCCCATTTGCCCGGGCTAAG	1620
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Db	1621	TGACTGCCACCTCCCGGCTGAC	ACTCACCACCTGCTGACCCCGGGGCTTCTCTGCGG	1680
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Db	1681	CCCTCGGCGAGCTGCTGAGAA	AGCCGAGCTGAGCGTCTCCACCGAGGCCCGAGT	1740
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QY	1861	GCCCCGGGAGAGAGCGGACAC	CCCGCGCGCGGCGACCTGCTGAGGCGCGCTACATT	1920
Db	1861	GCCCCGGGAGAGAGCGGACAC	CCCGCGCGCGGCGACCTGCTGAGGCGCGCTACATT	1920
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Db	2041	CGGCTGCTGCTCTGSCACCC	ACTTGGCCCCCTGGCCACAGCCACTCCCTTGGAAACATGAC	2100
QY	2101	TCTCCGAGCACCCCGCCCTCT	CTCGAGGCTGCGGTGAGGCAAGCGACTGCGCTTCA	2160
Db	2101	TCTCCGAGCACCCCGCCCTCT	CTCGAGGCTGCGGTGAGGCAAGCGACTGCGCTTCA	2160
QY	2161	GCCCCCTCCGGGGGGCCCCCT	TATCAGGGACATGGGGCACCTCAGGGCTCCAAAGCAGCTT	2220
Db	2161	GCCCCCTCCGGGGGGCCCCCT	TATCAGGGACATGGGGCACCTCAGGGCTCCAAAGCAGCTT	2220
QY	2221	CCATCCACTGTGTGGCCACCC	AGGCACTGTCTAGCCAGAGGCGCATCCCGGACAGGCTT	2280
Db	2221	CCATCCACTGTGTGGCCACCC	AGGCACTGTCTAGCCAGAGGCGCATCCCGGACAGGCTT	2280
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Db	2281	TGGGGGAGCAGCCCTTTCTG	CCACCCCAAGCAGGGTTCTGCCCCCGGAGGGGCTGC	2340
QY	2341	AGCCCCCACCCAGCAGTTG	CCCCCATGCCCCCTCTTCTCCCTCCAGGATCTTGCAA	2400

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4741 ACAGACATCTGGGCACTGGGTGACAGCTTCATCATGCTGAGCGCCGAGTACCGGGTG 4800
4741 ACAGACATCTGGGCACTGGGTGACAGCTTCATCATGCTGAGCGCCGAGTACCGGGTG 4800
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4801 AGCAGCGAGGTGACAGCGACTTCGAGAGGAGTGGCGCAAGGGGCTGTTCGGGCTGAGC 4860
4801 AGCAGCGAGGTGACAGCGACTTCGAGAGGAGTGGCGCAAGGGGCTGTTCGGGCTGAGC 4860
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4861 CGCTGCTACGGGGGGCTGCGGGGGGGCGCGTGGCGCTTCCTGGCGAGCACTCTGTGGCC 4920
4861 CGCTGCTACGGGGGGCTGCGGGGGGGCGCGTGGCGCTTCCTGGCGAGCACTCTGTGGCC 4920
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4921 CAGCCCTGGGGCCGGCCCTCGCGCTCCAGCTGCTGAGTGGCGCGCTGCTGAGGAGGAG 4980
4921 CAGCCCTGGGGCCGGCCCTCGCGCTCCAGCTGCTGAGTGGCGCGCTGCTGAGGAGGAG 4980
|||||
4981 GCGCGGGCTTCGCGCGCGCGCGCGCTGAGCTTCCTGAGCGCGGGCTGGCGCTTC 5040
4981 GCGCGGGCTTCGCGCGCGCGCGCGCTGAGCTTCCTGAGCGCGGGCTGGCGCTTC 5040
|||||
5041 GTGCGCAATCGAGAGAGAGCGCGCTGCTGTAACAAGAGCAACAACCTGGCCCGAGGTG 5100
5041 GTGCGCAATCGAGAGAGAGCGCGCTGCTGTAACAAGAGCAACAACCTGGCCCGAGGTG 5100
|||||
5101 CGCTGAGGCTGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
5101 CGCTGAGGCTGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
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5161 CAATAAAACGACAGCGCGCGCGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 5207
5161 CAATAAAACGACAGCGCGCGCGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 5207
|||||

RESULT 2

US-10-697-263-1
; Sequence 1, Application US/10697263
; Publication No. US20040063142A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000927-CIP-DIV2
; CURRENT APPLICATION NUMBER: US/10697,263
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 10/274,978
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-697-263-1

Query Match

100.0%; Score 5207; DB 13; Length 5207;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCAGAGGAACTCTTCTGATCACCCTGGCAGCTGAGGTGAGGTGGGAGAGCAGTG 60
DB 1 CAGCAGAGGAACTCTTCTGATCACCCTGGCAGCTGAGGTGAGGTGGGAGAGCAGTG 60
QY 61 GTTCCATTGAAGGAGTACTCCTAACTGTGTCAGAAAGCTGCGCGCTCAGGATGCGGGTGTGT 120
DB 61 GTTCCATTGAAGGAGTACTCCTAACTGTGTCAGAAAGCTGCGCGCTCAGGATGCGGGTGTGT 120
QY 121 CGCTTGGGCTGGGGGGGTTCAGTTCGCCACAGTGTATCTCAGGGTCTCACCACCAT 180
DB 121 CGCTTGGGCTGGGGGGGTTCAGTTCGCCACAGTGTATCTCAGGGTCTCACCACCAT 180
QY 181 CCAAGCATGCTAGGCTGTGGCTGGCACTGAGGCTGTTGCTGGGAGGAGTGTCTCCAC 240
DB 181 CCAAGCATGCTAGGCTGTGGCTGGCACTGAGGCTGTTGCTGGGAGGAGTGTCTCCAC 240
QY 241 AGTTCCCTCCCTGCGCTCCAGGGCCCGCATCCATGCAAGTAAACCATCGAGGATGTCGAG 300
DB 241 AGTTCCCTCCCTGCGCTCCAGGGCCCGCATCCATGCAAGTAAACCATCGAGGATGTCGAG 300
QY 301 GCA CAGCAGGCGGAAACCGCCCAATTCGAGGCTATCATTTGAGGGCGACCCACAGCCCTCG 360
DB 301 GCA CAGCAGGCGGAAACCGCCCAATTCGAGGCTATCATTTGAGGGCGACCCACAGCCCTCG 360
QY 361 GTGACCTGTGTAACAAGACAGCTGCGAGTGGTGGACAGCACCCCGCTTAGCAGCAGCAA 420
DB 361 GTGACCTGTGTAACAAGACAGCTGCGAGTGGTGGACAGCACCCCGCTTAGCAGCAGCAA 420
QY 421 GAAGGCAACACATATCTCCCTGGTGTGAGGCTATGAGGCTGCGAGGATGCGGGCTTTAC 480
DB 421 GAAGGCAACACATATCTCCCTGGTGTGAGGCTATGAGGCTGCGAGGATGCGGGCTTTAC 480
QY 481 ACCTGCTGCGCCCAAAAACACTGCTGGCGCAGGTGCTCTGCAAGGAGAGCTGCTGGTGT 540
DB 481 ACCTGCTGCGCCCAAAAACACTGCTGGCGCAGGTGCTCTGCAAGGAGAGCTGCTGGTGT 540
QY 541 GGGGGGGAACAATGAGCGGAGCTCAGAGAAAGAAAGCAACCGAGAGAGCTGCTCTCTTC 600
DB 541 GGGGGGGAACAATGAGCGGAGCTCAGAGAAAGAAAGCAACCGAGAGAGCTGCTCTCTTC 600
QY 601 TATGAGTCAAGGAGGAGATTGGAAGGGCGCTGTTGGCTTCGTAAGAGAGTGCAGCAC 660
DB 601 TATGAGTCAAGGAGGAGATTGGAAGGGCGCTGTTGGCTTCGTAAGAGAGTGCAGCAC 660
QY 661 AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCTCCCTACGAGGAGAGTCTGGGCC 720
DB 661 AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCTCCCTACGAGGAGAGTCTGGGCC 720
QY 721 CAGGCATACAGGAGGAGAGATCTTGGCGCGCTGAGCCACCCCGCTGAGTCTGAGGCTG 780
DB 721 CAGGCATACAGGAGGAGAGATCTTGGCGCGCTGAGCCACCCCGCTGAGTCTGAGGCTG 780
QY 781 CTGGACCACTTTGAGACCGCGCAAGACCTCATCTCTGAGTCTGAGTCTGCTCTATCCGAG 840
DB 781 CTGGACCACTTTGAGACCGCGCAAGACCTCATCTCTGAGTCTGAGTCTGCTCTATCCGAG 840
QY 841 GAGCTGCTGGAACCGCTGTACAGGAAGGGCGTGTGAGCGAGGGCCGAGGTCAGGTCCTAC 900
DB 841 GAGCTGCTGGAACCGCTGTACAGGAAGGGCGTGTGAGCGAGGGCCGAGGTCAGGTCCTAC 900
QY 901 ATCCAGCAGCTGCTGAGGGGCTGCACTACCTGACAGCCATGCGCTTCTCCACCTGAC 960
DB 901 ATCCAGCAGCTGCTGAGGGGCTGCACTACCTGACAGCCATGCGCTTCTCCACCTGAC 960
QY 961 ATAAAGCCCTCTAAACATCTCTGATGTCATCTCTCCCGGGAAGACATTAATAATCTGCGAC 1020
DB 961 ATAAAGCCCTCTAAACATCTCTGATGTCATCTCTCCCGGGAAGACATTAATAATCTGCGAC 1020
QY 1021 TTGSGCTTGGCCCAACATCAACCCAGCAGCTGCAAGTTCAGCCAGTACGGCTCCCT 1080
DB 1021 TTGSGCTTGGCCCAACATCAACCCAGCAGCTGCAAGTTCAGCCAGTACGGCTCCCT 1080

1021 TTGTGGTTTGGCCAGAAACATCACCCAGCAGAGTTCAGTTCAGCCAGTACGGTCCCTT 1080
1081 GAGTTCTGCTCCCGGAGATCATCAGCAGAACCTCTGTAGCGAAGCCTCCGACATTTGG 1140
1081 GAGTTCTGCTCCCGGAGATCATCAGCAGAACCTCTGTAGCGAAGCCTCCGACATTTGG 1140
1141 GCATGGGTGATCTCTACTCAGCTGACCTGACTCTATCCCAATTTGCGCGAGAGT 1200
1141 GCATGGGTGATCTCTACTCAGCTGACCTGACTCTATCCCAATTTGCGCGAGAGT 1200
1201 GACCTGACACCTCTCTGAAAGTCTCTGAGGGGGCGTGTATGAGCAGCCCATGGCT 1260
1201 GACCTGACACCTCTCTGAAAGTCTCTGAGGGGGCGTGTATGAGCAGCCCATGGCT 1260
1261 GCCACCTCAGGAGAGCCCAAGACTTCAACAGGCTACGCTGAGAGAGCCCTCAG 1320
1261 GCCACCTCAGGAGAGCCCAAGACTTCAACAGGCTACGCTGAGAGAGCCCTCAG 1320
1321 GCCGGGCTAGTGGGGCCAGTGGCTCTCCCAACCCCTGGTTCTGAAATCCATGCTGG 1380
1321 GCCGGGCTAGTGGGGCCAGTGGCTCTCCCAACCCCTGGTTCTGAAATCCATGCTGG 1380
1381 GAGGAGGCCACTTATCAACACCAAGAGCTCAAGTTCTCTGCGCCGGAAGTCCCTGG 1440
1381 GAGGAGGCCACTTATCAACACCAAGAGCTCAAGTTCTCTGCGCCGGAAGTCCCTGG 1440
1441 CAGGCTTCCCTGATGAGCTACAAGTCCATCCTGGTGTGCGCTCCATCCCTGAGCTGCTG 1500
1441 CAGGCTTCCCTGATGAGCTACAAGTCCATCCTGGTGTGCGCTCCATCCCTGAGCTGCTG 1500
1501 GGGGGCCACCGCAGCCCTCCCTGGCGTAGCCGCGACCTCTCAGGAGACATGGT 1560
1501 GGGGGCCACCGCAGCCCTCCCTGGCGTAGCCGCGACCTCTCAGGAGACATGGT 1560
1561 GGCCTCTCAGTTCCTCTCTCTGACAAAGAGCTCGCCCATTTGCGCGGCTAAG 1620
1561 GGCCTCTCAGTTCCTCTCTCTGACAAAGAGCTCGCCCATTTGCGCGGCTAAG 1620
1621 TCACCTGACACCTCCCGGTGACACACTCACCAGCTGTCGACCCCGGGCTTCCTGGCG 1680
1621 TCACCTGACACCTCCCGGTGACACACTCACCAGCTGTCGACCCCGGGCTTCCTGGCG 1680
1681 CCCTCGGCAGCTGCTCTGAGAAAGCCAGGAGCTCGCCCATTTGCGCGGCTAAG 1740
1681 CCCTCGGCAGCTGCTCTGAGAAAGCCAGGAGCTCGCCCATTTGCGCGGCTAAG 1740
1741 CGGCTGATCTCCGAGGGTCCGGGACCGGCGGCGGCGGCTGCGTCCCGGGCAG 1800
1741 CGGCTGATCTCCGAGGGTCCGGGACCGGCGGCGGCGGCTGCGTCCCGGGCAG 1800
1801 AGCGTATCCGAGCCTGTTCTACCAACAGGCGGTGAGAGCCCTGAGCAGCGGGCCCTG 1860
1801 AGCGTATCCGAGCCTGTTCTACCAACAGGCGGTGAGAGCCCTGAGCAGCGGGCCCTG 1860
1861 GCCCGGGAGAGCGGCGCACCGGCGGCGGCGGCGGCTGCTGAGAGGGGCTACATT 1920
1861 GCCCGGGAGAGCGGCGCACCGGCGGCGGCGGCGGCGGCTGCTGAGAGGGGCTACATT 1920
1921 GGGGGGGCTGCGCAGGCTGCGGAGCCACTGATGAGCAGCCGCGTGTGAGAGGAGGAG 1980
1921 GGGGGGGCTGCGCAGGCTGCGGAGCCACTGATGAGCAGCCGCGTGTGAGAGGAGGAG 1980
1981 GCGCGCAGGAGAGCAGGCGACCTCTCTGCGCAAGCCGCGCTCATTCGAGACTGCGCTC 2040
1981 GCGCGCAGGAGAGCAGGCGACCTCTCTGCGCAAGCCGCGCTCATTCGAGACTGCGCTC 2040
2041 CGGCTGCTCTGCGCTGCGCAGCCACTTGGCCCTCGGCCACAGCCACTCCCTGGAACATGAC 2100
2041 CGGCTGCTCTGCGCTGCGCAGCCACTTGGCCCTCGGCCACAGCCACTCCCTGGAACATGAC 2100
2101 TCTCCGAGCAGCCCGGCGCTCTCTGAGAGGCTCTGCGGTGAGGAGCAGGAGCTGCGCTCA 2160
2101 TCTCCGAGCAGCCCGGCGCTCTCTGAGAGGCTCTGCGGTGAGGAGCAGGAGCTGCGCTCA 2160

2161 GCCCCTCTCCGGGGGGCCCTATCAGGGACATGGGGCACCTCAGGGCTCCAAAGCAGCTT 2220
2161 GCCCCTCTCCGGGGGGCCCTATCAGGGACATGGGGCACCTCAGGGCTCCAAAGCAGCTT 2220
2221 CCATCCACTGGTGGCCACCCAGGACATGCTCAGCGCAGAGGGCATCCCGGACACCCCT 2280
2221 CCATCCACTGGTGGCCACCCAGGACATGCTCAGCGCAGAGGGCATCCCGGACACCCCT 2280
2281 TGGGGGAGCAGCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGC 2340
2281 TGGGGGAGCAGCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGC 2340
2341 AGCCCCCAACAGCAGTGGCCCATGCTCTGCTGCTCTCTCTCCCTCAGAGTCTTGCATA 2400
2341 AGCCCCCAACAGCAGTGGCCCATGCTCTGCTGCTCTCTCTCCCTCAGAGTCTTGCATA 2400
2401 GAGGCCCTCTTAGTACCTCAAGCCCTCTTCTGGGACAGCCCGGACAGCCCTGCGCCCT 2460
2401 GAGGCCCTCTTAGTACCTCAAGCCCTCTTCTGGGACAGCCCGGACAGCCCTGCGCCCT 2460
2461 GCCAAAGCAGCCCTTGGACTCTAGATGGGGCTTGGAGACATCTCTCTCTCTGGG 2520
2461 GCCAAAGCAGCCCTTGGACTCTAGATGGGGCTTGGAGACATCTCTCTCTCTGGG 2520
2521 AGGCCAAAACCCGGCCCTGCTGAGTTCCCAAGGCTCAGCTCCCAAGCAGCTCTTCCCAA 2580
2521 AGGCCAAAACCCGGCCCTGCTGAGTTCCCAAGGCTCAGCTCCCAAGCAGCTCTTCCCAA 2580
2581 GTGAGCTCCCTCAGGGTGGGCTCTCTCCAGGTGGGACAGAGGCTGGCCCTCCCTGGAT 2640
2581 GTGAGCTCCCTCAGGGTGGGCTCTCTCCAGGTGGGACAGAGGCTGGCCCTCCCTGGAT 2640
2641 GCGAGAGGCTGGACCCAGGAGGTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCG 2700
2641 GCGAGAGGCTGGACCCAGGAGGTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCG 2700
2701 CCTCAGAGCAGGTGACCATGCGCAAGTTCTCCTCGGTGCTCGGGGGCTACGACAGC 2760
2701 CCTCAGAGCAGGTGACCATGCGCAAGTTCTCCTCGGTGCTCGGGGGCTACGACAGC 2760
2761 GTGCTGCTATGCGACCTTTGCTTGTGTGAGATGTCAGGGGGGCAATGTGCGGGCAGGG 2820
2761 GTGCTGCTATGCGACCTTTGCTTGTGTGAGATGTCAGGGGGGCAATGTGCGGGCAGGG 2820
2821 CCCATGCGGCGCAGGATAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
2821 CCCATGCGGCGCAGGATAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
2881 GCCAGGCTGAGTCCCAAGTCCGAGGAGCAGCAGGAGCCAGGGCTGAGAGCCACTGCGC 2940
2881 GCCAGGCTGAGTCCCAAGTCCGAGGAGCAGCAGGAGCCAGGGCTGAGAGCCACTGCGC 2940
2941 CAGGTCACTGCAAGGCTGCTGCTGAGTGGCGCAGGGCTCCCAAGGAGGCTTCCAGAG 3000
2941 CAGGTCACTGCAAGGCTGCTGCTGAGTGGCGCAGGGCTCCCAAGGAGGCTTCCAGAG 3000
3001 CCCACCCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGACCTGTCAAGT 3060
3001 CCCACCCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGACCTGTCAAGT 3060
3061 GATCGGAGGCGGCGGACACATATCCCTGGAATTCGAGGTGGACCCCGCTACCTC 3120
3061 GATCGGAGGCGGCGGACACATATCCCTGGAATTCGAGGTGGACCCCGCTACCTC 3120
3121 AACCTCTCAGACCTGTACGATATCAAGTACCTCCCAATTCGAGTTTATGATCTTCAAGAAA 3180
3121 AACCTCTCAGACCTGTACGATATCAAGTACCTCCCAATTCGAGTTTATGATCTTCAAGAAA 3180
3181 GTCCCCAAGTCCCTCAGCCAGAGCCCTCCCTCCCATGCTGAGGAGGAGCTGCGCCGAG 3240
3181 GTCCCCAAGTCCCTCAGCCAGAGCCCTCCCTCCCATGCTGAGGAGGAGCTGCGCCGAG 3240

[illegible]

RESULT 3

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RESULT 3
US-10-697-263-3
; Sequence 3, Application US/10697263
; Publication NO. US20040063142A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROCD
; FILE REFERENCE: C4000927-CIP-DIV2
; CURRENT APPLICATION NUMBER: US/10/697,263
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 10/274,978

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; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-697-263-3

Query Match
Best Local Similarity 100.0%; Score 5207; DB 13; Length 5207;
Matches 5207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGAGAGAACTCTCTCTGATCACTGGCCAGCTGAGGTCAAGTGGAGAGGAGTGG 60
DB 1 CAGCAGAGAGAACTCTCTCTGATCACTGGCCAGCTGAGGTCAAGTGGAGAGGAGTGG 60
QY 61 GTTCCATTGAAGAGAGTACTCTTAATGTCAAGAGCTGGGCGGTCAAGATGGGGTCTGT 120
DB 61 GTTCCATTGAAGAGAGTACTCTTAATGTCAAGAGCTGGGCGGTCAAGATGGGGTCTGT 120
QY 121 GCTTGGGCTGCGGGGGTGTTCAGTTGGCCCAAGTGTATCTCAGGGTCTCAACCAAT 180
DB 121 GCTTGGGCTGCGGGGGTGTTCAGTTGGCCCAAGTGTATCTCAGGGTCTCAACCAAT 180
QY 181 CCAAGCATGTAGGTGTGGCTGCACACCAAGGGTGTGTGGCTGGGAGGTGTCTCCAC 240
DB 181 CCAAGCATGTAGGTGTGGCTGCACACCAAGGGTGTGTGGCTGGGAGGTGTCTCCAC 240
QY 241 AGTTCCCTCCCTCCAGGCGCCCATTCATGCAAGTAAACATTCAGAGATGTCAG 300
DB 241 AGTTCCCTCCCTCCAGGCGCCCATTCATGCAAGTAAACATTCAGAGATGTCAG 300
QY 301 GCACAGACAGCGGAAAGCGCCCAATTCGAGGCTATCATTCAGGGCGACCAAGCCCTCG 360
DB 301 GCACAGACAGCGGAAAGCGCCCAATTCGAGGCTATCATTCAGGGCGACCAAGCCCTCG 360
QY 361 GTGACCTGTACAGGACAGGCTCCAGTGGTGGACAGACACCGGCTTACAGCAGAGCA 420
DB 361 GTGACCTGTACAGGACAGGCTCCAGTGGTGGACAGACACCGGCTTACAGCAGAGCA 420
QY 421 GAAGSCACCACTACTCCCTGGTGTGAGGCATGTGGGCTTCAAGAGATGCGGCGTTTAC 480
DB 421 GAAGSCACCACTACTCCCTGGTGTGAGGCATGTGGGCTTCAAGAGATGCGGCGTTTAC 480
QY 481 ACCTGCTGGCCCAACACTGTGGGCGAGTGTCTGCAAGCAGAGCTGTGTGTGT 540
DB 481 ACCTGCTGGCCCAACACTGTGGGCGAGTGTCTGCAAGCAGAGCTGTGTGTGT 540
QY 541 GGGGGGACAAATGAGCCGGACTCAGAGAAGCAAGCCACCGAGGAGAGTGCACCTCTTC 600
DB 541 GGGGGGACAAATGAGCCGGACTCAGAGAAGCAAGCCACCGAGGAGAGTGCACCTCTTC 600
QY 601 TATGAGGTCAAGGAGAGATGGAGGGGGTGTGGCTTGTGCTTAAAGAGTGCAGCAC 660
DB 601 TATGAGGTCAAGGAGAGATGGAGGGGGTGTGGCTTGTGCTTAAAGAGTGCAGCAC 660
QY 661 AAAGGAAACAGATCTTGTGGCTGCAAGTTCATCCCCCTACGAGCAGAACTCGGGCC 720
DB 661 AAAGGAAACAGATCTTGTGGCTGCAAGTTCATCCCCCTACGAGCAGAACTCGGGCC 720
QY 721 CAGGATACAGGAGAGAGATCTCTGGGCGGCTGAGCCACCGGCTGTGTACAGGGCTG 780
DB 721 CAGGATACAGGAGAGAGATCTCTGGGCGGCTGAGCCACCGGCTGTGTACAGGGCTG 780
QY 781 CTGACACAGTTTGAGACCCCGCAGACCCCTCATCTCTGAGGTGTGTCTATCCGAG 840
DB 781 CTGACACAGTTTGAGACCCCGCAGACCCCTCATCTCTGAGGTGTGTCTATCCGAG 840

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QY 841 GAGTGTGTGACCCCTGTGTACAGGAAGGGCGTGTGACCGAGGCCGAGGTCAAGGTCTAC 900
DB 841 GAGTGTGTGACCCCTGTGTACAGGAAGGGCGTGTGACCGAGGCCGAGGTCAAGGTCTAC 900
QY 901 ATCCAGCAGCTGTGTGAGGGGCTGCACTACCTGCAAGCAGCATGGCTTCTCCACCTGGAC 960
DB 901 ATCCAGCAGCTGTGTGAGGGGCTGCACTACCTGCAAGCAGCATGGCTTCTCCACCTGGAC 960
QY 961 ATAAAGCCCTCTAACTCTCTGATGTGCACTCTGCGGGGAAAGACATTTAAATCTCTGCGAC 1020
DB 961 ATAAAGCCCTCTAACTCTCTGATGTGCACTCTGCGGGGAAAGACATTTAAATCTCTGCGAC 1020
QY 1021 TTTGGCTTTTCCAGAAACATCACCCAGCAGAGCTCAGTTTCAAGCCAGTACGGCTCCCTCT 1080
DB 1021 TTTGGCTTTTCCAGAAACATCACCCAGCAGAGCTCAGTTTCAAGCCAGTACGGCTCCCTCT 1080
QY 1081 GAGTTCGTCTCTCCCGAGATTCACAGCAACCTCTGTGAGCAAGCCCTCCGACATTTGG 1140
DB 1081 GAGTTCGTCTCTCCCGAGATTCACAGCAACCTCTGTGAGCAAGCCCTCCGACATTTGG 1140
QY 1141 GGCATGGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
DB 1141 GGCATGGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201 GACGTGCCACCTCTCTGAAAGCTCTGTGAGGGGGCGGTGTCTATGAGCAGAGCCCAATGGCT 1260
DB 1201 GACGTGCCACCTCTCTGAAAGCTCTGTGAGGGGGCGGTGTCTATGAGCAGAGCCCAATGGCT 1260
QY 1261 GCCCACCCTCAGCAAGCAAGCAAGCAAGCTTCACTCAAGGCTTCACTCAAGGCTTCACTCA 1320
DB 1261 GCCCACCCTCAGCAAGCAAGCAAGCAAGCTTCACTCAAGGCTTCACTCAAGGCTTCACTCA 1320
QY 1321 GCGCGGCTAGTGGCGGCGAGTGTCTCTCCACCCCTGGTTCCTGAAATCCATGCTGCTG 1380
DB 1321 GCGCGGCTAGTGGCGGCGAGTGTCTCTCCACCCCTGGTTCCTGAAATCCATGCTGCTG 1380
QY 1381 GAGGAGGCGGCTCTCTCAACCAAGCAGCTCAAGTTCCTCTGCGGCGGAGTGGCTGG 1440
DB 1381 GAGGAGGCGGCTCTCTCAACCAAGCAGCTCAAGTTCCTCTGCGGCGGAGTGGCTGG 1440
QY 1441 CAGCGTTCCTGTATGAGTCAAGTCCATCTCTGTGTGATGGCTTCATCTCTGAGTGTG 1500
DB 1441 CAGCGTTCCTGTATGAGTCAAGTCCATCTCTGTGTGATGGCTTCATCTCTGAGTGTG 1500
QY 1501 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560
DB 1501 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560
QY 1561 GGTCTCTCAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
DB 1561 GGTCTCTCAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
QY 1621 TCACTGCCACCTCTCCCGGTGACACACTCACCCTGCTGCAACCGGCGGCTTCTCTGCGG 1680
DB 1621 TCACTGCCACCTCTCCCGGTGACACACTCACCCTGCTGCAACCGGCGGCTTCTCTGCGG 1680
QY 1681 CCTCTCGGCGGCTGCTGAGGAGCGGAGCGGAGCGGCTCCACCGAGGCCCGGCTTCTCTG 1740
DB 1681 CCTCTCGGCGGCTGCTGAGGAGCGGAGCGGAGCGGCTCCACCGAGGCCCGGCTTCTCTG 1740
QY 1741 CCGCTCTGCTCTCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1800
DB 1741 CCGCTCTGCTCTCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1800
QY 1801 AGGCTCATCCGAGCTGTCTTACCAAGGCGGCTGAGAGCGGCTGAGCAGCGGCGGCTG 1860
DB 1801 AGGCTCATCCGAGCTGTCTTACCAAGGCGGCTGAGAGCGGCTGAGCAGCGGCGGCTG 1860
QY 1861 GCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1920
DB 1861 GCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1920
QY 1921 GCGGGGCGGCTGCCAGGCTGCGCGGAGCCAATGATGAGACACCGGCTCTGAGGAGGAG 1980

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RESULT 4
US-10-415-011-44
; Sequence 44, Application US/10415011
; Publication No. US2004003394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: RAO, Monique G.
; APPLICANT: RAMKUNAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: BOSOMSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCN/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 5454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US200400
US-10-415-011-44
Query Match 99.4%; Score 5173
Best Local Similarity 99.8%; Pred. No.
Matches 5179; Conservative 0; Mismatch

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Query Match	99.4%	Score 5173.6	DB 13	Length 5454
Best Local Similarity	99.8%	Pred. No. 0		
Matches 5179	Conservative 0	Mismatches 9	Indels 0	Gaps 0
QY	3	GCACAGGACTCTCTCTGATCACCCTGAGTTCAGATGGGAGAGGACGATGGT	62	

QY 63 TCCATTGAAGAGTACTCTAACTGTGAGAGGCTGGCGGTGAGGATGGGTGCTGTCG 122
DB 327 TCCATTGAAGAGTACTCTAACTGTGAGAGGCTGGCGGTGAGGATGGGTGCTGTCG 386
QY 123 CTTCGGCTGGGGGGTTCAGTTCGCCACAGTGTATCTCAGGTCCTCACCACATCC 182
DB 387 CTTCGGCTGGGGGGTTCAGTTCGCCACAGTGTATCTCAGGTCCTCACCACATCC 446
QY 183 AAGCATGGTAGGTGTGGCTGGACCCAGGGTGTGTGCTGGGGAGTGTCTCCACAG 242
DB 447 AAGCATGGTAGGTGTGGCTGGACCCAGGGTGTGTGCTGGGGAGTGTCTCCACAG 506
QY 243 TTCCCTCCCTCCCTCCAGGGCCCATCATGACAGGTAAACATGAGGATGTGCGAGC 302
DB 507 TTCCCTCCCTCCCTCCAGGGCCCATCATGACAGGTAAACATGAGGATGTGCGAGC 566
QY 303 ACAGACAGGGGAAACGGCCCAATTCGAGGCTATPCATTTGAGGCGACCCACAGCCCTCGGT 362
DB 567 ACAGACAGGGGAAACGGCCCAATTCGAGGCTATPCATTTGAGGCGACCCACAGCCCTCGGT 626
QY 363 GACCTGTGTAAGGACAGCGCTCAGCTGTGTGACAGCACCCGGCTTAGCGACGACRAGA 422
DB 627 GACCTGTGTAAGGACAGCGCTCAGCTGTGTGACAGCACCCGGCTTAGCGACGACRAGA 686
QY 423 AGGCACACATPACTCTCTGTGTGTGAGGCAATGTGGCTCGAAGGATGCGGCTTTACAC 482
DB 687 AGGCACACATPACTCTCTGTGTGTGAGGCAATGTGGCTCGAAGGATGCGGCTTTACAC 746
QY 483 CTGCTGTGCCCCAAACACTGCTGTGCGCAGGTGCTCTGCAAGGACAGCTGCTGTGCTGG 542
DB 747 CTGCTGTGCCCCAAACACTGCTGTGCGCAGGTGCTCTGCAAGGACAGCTGCTGTGCTGG 806
QY 543 GGGGGAACAATGAGCGGACTTCAGAGAAAGCAAGCCACCGGAGGAAAGTGCATCTCTCTA 602
DB 807 GGGGGAACAATGAGCGGACTTCAGAGAAAGCAAGCCACCGGAGGAAAGTGCATCTCTCTA 866
QY 603 TGAGGTCAAGGAGGAGATTCGAAAGGGCGTGTGTGCTTCGTAAGGAGTGCACACAA 662
DB 867 TGAGGTCAAGGAGGAGATTCGAAAGGGCGTGTGTGCTTCGTAAGGAGTGCACACAA 926
QY 563 AGGAAAACAAGATTTGTGCGCTGCCAAGTTCACTCCCTCTACCGGAGCAAACTCGGGGCCA 722
DB 927 AGGAAAACAAGATTTGTGCGCTGCCAAGTTCACTCCCTCTACCGGAGCAAACTCGGGGCCA 986
QY 723 GGCATACAGGAGCGAGACATCTGCGCGCTGTGAGCCACCGCTGTGTCAAGGGGCTGCT 782
DB 987 GGCATACAGGAGCGAGACATCTGCGCGCTGTGAGCCACCGCTGTGTCAAGGGGCTGCT 1046
QY 783 GGACAGTTTGAGCCCGGAAGACCCCTCATCTCATCTCTGAGCTGTGCTATCCGAGGA 842
DB 1047 GGACAGTTTGAGCCCGGAAGACCCCTCATCTCATCTCTGAGCTGTGCTATCCGAGGA 1106
QY 843 GCTGCTGACCGGCTGTACAGGAGGGCGTGTGTGACGAGGCGCGAGGTCAAGGTCTACAT 902
DB 1107 GCTGCTGACCGGCTGTACAGGAGGGCGTGTGTGACGAGGCGCGAGGTCAAGGTCTACAT 1166
QY 903 CCAGCAGCTGGTGAAGGGGTGCACTACTGTGACAGCCATGGCGTTCTCCACCTGGACAT 962
DB 1167 CCAGCAGCTGGTGAAGGGGTGCACTACTGTGACAGCCATGGCGTTCTCCACCTGGACAT 1226
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DB 1227 AAAGCCCTCTAAATCTGTATGTGTGATCTGTGCGGGAAGACATTAATAATCTGCGACTT 1286
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QY 1083 GTTCGTCTCCCGAGATCATCCAGAGAACCCCTGTGAGCGAAGCCCTCCGACATTTGGGC 1142
DB 1347 GTTCGTCTCCCGAGATCATCCAGAGAACCCCTGTGAGCGAAGCCCTCCGACATTTGGGC 1406
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DB 1407 CATGGGTGTCTCTCTACCTAGCCTGACCTGCTCATCCCCATTTGCGCGGAGAGTGA 1466
QY 1203 CCGTGCACCCCTCTGAGAGTCTCTGGAGGGGGGTGTATGGAGCAGCCCCCATGGGTGC 1262
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QY 1263 CCACCTCAGCGAAGACGCGCAAGAGCTTCATCAAGGCTACGCTGAGAGAGAGCCCTCAGGC 1322
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QY 1323 CCGGCTAGTGGCGGCCAGTGCCTCTCCACCCCTGTTCTGAAATCCATGCTGCGGA 1382
DB 1587 CCGGCTAGTGGCGGCCAGTGCCTCTCCACCCCTGTTCTGAAATCCATGCTGCGGA 1646
QY 1383 GGAGGCCACTTTCAATCAACCAAGAGCTCAAGTTCCTCTGCGCCGAAAGTTCGCTGGCA 1442
DB 1647 GGAGGCCACTTTCAATCAACCAAGAGCTCAAGTTCCTCTGCGCCGAAAGTTCGCTGGCA 1706
QY 1443 GGTTCCTCTGATGAGTCAAGTCCATCTCTGATGCTGCTCCATCCTGTAGCTGCTGCG 1502
DB 1707 GGTTCCTCTGATGAGTCAAGTCCATCTCTGATGCTGCTCCATCCTGTAGCTGCTGCG 1766
QY 1503 GGGGCCACCGGACAGCCCTCTCTGCGGTAGCCGGGACCTCTGCAAGGACACTGTGTGG 1562
DB 1767 GGGGCCACCGGACAGCCCTCTCTGCGGTAGCCGGGACCTCTGCAAGGACACTGTGTGG 1826
QY 1563 CTCTCCAGTTCCTCTCTCTCTGACACAGCTGCGCCCATTTGCGCGGGCTAAGTC 1622
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DB 1887 ACTGCCACCTCTCCCGGTGACACACTCAGCTGCTGACACCCCGGGGCTCTCTGCGGCC 1946
QY 1683 CTCGCGCAGCTCTGCTGAGGAGGCGGAGCCAGTGTGAGCGTTCACACGAGGCCCTCAGCTCC 1742
DB 1947 CTCGCGCAGCTCTGCTGAGGAGGCGGAGCCAGTGTGAGCGTTCACACGAGGCCCTCAGCTCC 2006
QY 1743 GCTGCTATCTCCGAGGCTGCGGGCCACCGGCGCCGAGGCTGCTGCGCGGCGACAG 1802
DB 2007 GCTGCTATCTCCGAGGCTGCGGGCCACCGGCGCCGAGGCTGCTGCGCGGCGACAG 2066
QY 1803 CGTCTATCCGCGACCTCTTCTACCAAGCGGGGTGAGAGCCCTGAGCACGCGGGGCTTGGC 1862
DB 2067 CGTCTATCCGCGACCTCTTCTACCAAGCGGGGTGAGAGCCCTGAGCACGCGGGGCTTGGC 2126
QY 1863 CCGGGGAGCAGCGGCGACCCGGGCGCGGCGGCACTGCTGAAGGCGGCTACATTGC 1922
DB 2127 CCGGGGAGCAGCGGCGACCCGGGCGCGGCGGCACTGCTGAAGGCGGCTACATTGC 2186
QY 1923 GGGGGCGCTGCGCAGGCTTCTGCGGAGCCACTGATGAGGACACCGCGTGTGAGGAGGAGGC 1982
DB 2187 GGGGGCGCTGCGCAGGCTTCTGCGGAGCCACTGATGAGGACACCGCGTGTGAGGAGGAGGC 2246
QY 1983 CGCCAGGGAGGAGCAGCGGCGACCCCTCTGGCCAAAGCCCTCATTTGAGACTGCGCTCCG 2042
DB 2247 CGCCAGGGAGGAGCAGCGGCGACCCCTCTGGCCAAAGCCCTCATTTGAGACTGCGCTCCG 2306
QY 2043 GGTGCTGCTGCTGCGACCCCTTGGGCCCTGGCCACAGCCACTCTCCCTGGAACATGACTC 2102
DB 2307 GGTGCTGCTGCTGCGACCCCTTGGGCCCTGGCCACAGCCACTCTCCCTGGAACATGACTC 2366
QY 2103 TCGAGGACCCCGCGCCCTCTCTGAGGCTGCGGTGAGGACAGGAGTGCCTTCAGC 2162
DB 2367 TCGAGGACCCCGCGCCCTCTCTGAGGCTGCGGTGAGGACAGGAGTGCCTTCAGC 2426
QY 2163 CCGCTCCGGGGGGGGCCCTTATCAGGAGCATGGGGCACCCCTCAGGGCTCCAGGAGCTTCC 2222
DB 2427 CCGCTCCGGGGGGGGCCCTTATCAGGAGCATGGGGCACCCCTCAGGGCTCCAGGAGCTTCC 2486
QY 2223 ATCCACTGGTGGCGCACCGAGGACTGCTCAGCGAGAGGCGCATCCCGGACAGCCCTTG 2282

4443 CTCTGGGCGGAGCTGCTCCCTGCTGCGCGAGAGGCGCTCTACTCAGAACTCTGAGGT 4502
Db CTCTGGGCGGAGCTGCTCCCTGCTGCGCGAGAGGCGCTCTACTCAGAACTCTGAGGT 4766
4503 GAAGACTACTCTGTGGGAGATGTTGAGTGCCACCCAGTACTGTCAGAACAGACATCT 4562
Db GAAGACTACTCTGTGGGAGATGTTGAGTGCCACCCAGTACTGTCAGAACAGACATCT 4826
4563 GCACCTGAGACCTGAGTCCGAGAACATGATCATCACCGAATACAACTGCTCAAGTCT 4622
Db GCACCTGAGACCTGAGTCCGAGAACATGATCATCACCGAATACAACTGCTCAAGTCT 4886
4623 GCACCTGAGACCTGAGTCCGAGAACATGATCATCACCGAATACAACTGCTCAAGTCT 4692
Db GCACCTGAGACCTGAGTCCGAGAACATGATCATCACCGAATACAACTGCTCAAGTCT 4946
4683 GGACTACTAGAGACCTAGGCTCCAGAGAGCTCTGAGAGGCGCAGGGGCTGTTCCACAGAC 4742
Db GGACTACTAGAGACCTAGGCTCCAGAGAGCTCTGAGAGGCGCAGGGGCTGTTCCACAGAC 5006
4743 AGACATCTGGGCGCATCGGTGTGAGAGCTTCATGCTGAGCGCGAGTACCCGGTGAG 4802
Db AGACATCTGGGCGCATCGGTGTGAGAGCTTCATGCTGAGCGCGAGTACCCGGTGAG 5066
4803 CAGCAGAGGTGCACGCGACCTGCAGAGAGAGTGCAGAGGGGCTGCTCGGCTGAGCG 4862
Db CAGCAGAGGTGCACGCGACCTGCAGAGAGAGTGCAGAGGGGCTGCTCGGCTGAGCG 5126
4863 CTGCTACCGCGGCTGTCCGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4922
Db CTGCTACCGCGGCTGTCCGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5186
4923 GCGCTGGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4982
Db GCGCTGGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5246
4983 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5042
Db CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5306
5043 GCGCAATCGGAGAGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5102
Db GCGCAATCGGAGAGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5366
5103 CTGAGGGTCCGCGCGCGCGCACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5162
Db CTGAGGGTCCGCGCGCGCGCACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5426
5163 ATAAAGCGCAGCGCGCGCGAGAAAA 5190
Db ATAAAGCGCAGCGCGCGCGAGAAAA 5454

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US-10-077-130-1
; Sequence 1, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047PIRCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/249201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8106
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(71)
; NAME/KEY: CDS
; LOCATION: (72)...(7964)
; NAME/KEY: 3'UTR
; LOCATION: (7965)...(8106)
US-10-077-130-1

Query Match 94.9%; Score 4940.4; DB 14; Length 8106;
Match Local Similarity 99.9%; Pred. No. 0;
Matches 4944; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 258 CCAGGGGCCCCCATCCATGCGAGTAACCATGAGGATGTGCGAGGACAGACAGCGCGAAC 317
Db 3116 CGCACGGCCCCCATCCATGCGAGTAACCATGAGGATGTGCGAGGACAGACAGCGCGAAC 3175
Qy 318 GGGCCAAATTCGAGGCTATCATTTAGGGGACCCACAGCCCTCGGTGACCTGGGTACAGGA 377
Db 3176 GGGCCAAATTCGAGGCTATCATTTAGGGGACCCACAGCCCTCGGTGACCTGGGTACAGGA 3235
Qy 378 CAGCGTCCAGCTGTGTGGAAGCAGCAGCCCGGCTTAGCCAGCAGCAAGAGCCACCATATCTC 437
Db 3236 CAGCGTCCAGCTGTGTGGAAGCAGCAGCCCGGCTTAGCCAGCAGCAAGAGCCACCATATCTC 3295
Qy 438 CTTGTGTCTGAGGCTGTGGCTCGAGGATGCCGGGTTTACACCTGCTGCTGCCAAAA 497
Db 3296 CTTGTGTCTGAGGCTGTGGCTCGAGGATGCCGGGTTTACACCTGCTGCTGCCAAAA 3355
Qy 498 CACTGTGTCAGGCTGTCTGCAAGGACAGAGCTGCTGTGCTTGGGGGGGACAAATGAGCC 557
Db 3356 CACTGTGTCAGGCTGTCTGCAAGGACAGAGCTGCTGTGCTTGGGGGGGACAAATGAGCC 3415
Qy 558 GGAATCAG 617
Db 3416 GGAATCAG 3475
Qy 618 GATTGGAAGGGCGGTGTTGGCTTCTGTAAGAGAGTGCAGACAGAGAGAGAGAGAGAGAG 677
Db 3476 GATTGGAAGGGCGGTGTTGGCTTCTGTAAGAGAGTGCAGACAGAGAGAGAGAGAGAG 3535
Qy 678 GTGCGCTGCAAGTTTATCCCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737
Db 3536 GTGCGCTGCAAGTTTATCCCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3595
Qy 738 AGACATCTTGGCGCGCTGAGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Db 3596 AGACATCTTGGCGCGCTGAGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3655
Qy 798 CCGCAAGACCTCTATCTCTATCTCTGAGAGTGTGCTCATCCGAGAGAGTGTGCTGAGCCGCT 857
Db 3656 CCGCAAGACCTCTATCTCTATCTCTGAGAGTGTGCTCATCCGAGAGAGTGTGCTGAGCCGCT 3715
Qy 858 GTACAGGAGAGGCGGTGAG 917
Db 3716 GTACAGGAGAGGCGGTGAG 3775
Qy 918 GGGGCTGCACTACCTGCAAGCCATGCGGCTTCTCCACCTGGAACATAAGCCCTCTAACAT 977
Db 3776 GGGGCTGCACTACCTGCAAGCCATGCGGCTTCTCCACCTGGAACATAAGCCCTCTAACAT 3835
Qy 978 CTTGATGTGTGATCTCTGCGCGGAGAGACATTTAAATCTGCGACTTTGGCTTTGCCAGAA 1037
Db 3836 CTTGATGTGTGATCTCTGCGCGGAGAGACATTTAAATCTGCGACTTTGGCTTTGCCAGAA 3895
Qy 1038 CATCAACCCAG 1097
Db 3896 CATCAACCCAG 3955
Qy 1098 GATCATCCAG 1157
Db 3956 GATCATCCAG 4015

Qy	4443	CTCTGGGCCCGAGCTGCCTCCCTGCCCTGGCCGAGAGGGCTCTCTACTCAGAACTCGAGGT	4502
Db	4707	CTCTGGGCCCGAGCTGCCTCCCTGCCCTGGCCGAGAGGGCTCTCTACTCAGAACTCCGAGGT	4766
Qy	4503	GAAGACTACCTGTGGCAGATGTTGAGTGCACCCACAGTACCTGCACACACAGACACATCCCT	4562
Db	4767	GAAGACTACCTGTGGCAGATGTTGAGTGCACCCACAGTACCTGCACACACAGACACATCCCT	4826
Qy	4563	GCACCTGGACCTGAGGCTCCGAGAACATGATCATCAACCGAATAACAACCTGCTCAAGGTCGT	4622
Db	4827	GCACCTGGACCTGAGGCTCCGAGAACATGATCATCAACCGAATAACAACCTGCTCAAGGTCGT	4886
Qy	4623	GGACCTGGCCAAATGCACAGAGCTCCAGCCAGGAGAGGTGCTGCCCTCAGACAGATTCAA	4682
Db	4887	GGACCTGGCCAAATGCACAGAGCTCCAGCCAGGAGAGGTGCTGCCCTCAGACAGATTCAA	4946
Qy	4683	GGACTACCTAGAGACCAATGGTCCAGAGCTCTGGAGGCCAAGGGGGTGTTTCCACAGAC	4742
Db	4947	GGACTACCTAGAGACCAATGGTCCAGAGCTCTGGAGGCCAAGGGGGTGTTTCCACAGAC	5006
Qy	4743	AGACATCTGGGCCCATCGTGTGACAGCTTCATCATGCTGAGCGCCGAGTACCCGGTGAG	4802
Db	5007	AGACATCTGGGCCCATCGTGTGACAGCTTCATCATGCTGAGCGCCGAGTACCCGGTGAG	5066
Qy	4803	CAGCAGAGGTCGACGGACCTGCAGAGAGGAGTGGCAAGGGGGTGTTTCGGGTGAGCCG	4862
Db	5067	CAGCAGAGGTCGACGGACCTGCAGAGAGGAGTGGCAAGGGGGTGTTTCGGGTGAGCCG	5126
Qy	4863	CTGCTACGCGGGGCTGTCCGGGGGCGCGTGGACCTTCCTGGCGACATCTGTGGCGCCA	4922
Db	5127	CTGCTACGCGGGGCTGTCCGGGGGCGCGTGGACCTTCCTGGCGACATCTGTGGCGCCA	5186
Qy	4923	GGCTTGGGGCCGGCCCTGGCGCTCCAGCTGCTCGAGTGCCTGGTGTAAACAGAGAGGG	4982
Db	5187	GGCTTGGGGCCGGCCCTGGCGCTCCAGCTGCTCGAGTGCCTGGTGTAAACAGAGAGGG	5246
Qy	4983	CCCGGCTGTTCGGGGCCCGCGCCGTGACCTTCCTACCGCGGGCTGGCGCTCTTCGT	5042
Db	5247	CCCGGCTGTTCGGGGCCCGCGCCGTGACCTTCCTACCGCGGGCTGGCGCTCTTCGT	5306
Qy	5043	GGCCAAATCGCAGAGAGACGCGCGCTGTGTGTAAGAGGGCAACAACCTGGGCCAGGTGGG	5102
Db	5307	GGCCAAATCGCAGAGAGACGCGCGCTGTGTGTAAGAGGGCAACAACCTGGGCCAGGTGGG	5366
Qy	5103	CTGAGGGTCGCCCCCGGCCACAACCTTGGTCTCCCGCTGGGGGTTGCTGCAGACGCGCCA	5162
Db	5367	CTGAGGGTCGCCCCCGGCCACAACCTTGGTCTCCCGCTGGGGGTTGCTGCAGACGCGCCA	5426
Qy	5163	ATATAAAGCGACACCGCGGGCGAGAAAA	5190
Db	5427	ATATAAAGCGACACCGCGGGCGAGAAAA	5454

RESULT 5

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RESULTS 5
US-10-077-130-1
/ Sequence 1, Application US/10077130
/ Publication NO. US20020168742A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapeller-Libermann, Rosana
/ APPLICANT: Acton, Susan L.
/ TITLE OF INVENTION: 53079 and 12599, Protein Kinase Family
/ TITLE OF INVENTION: Members and Uses Therefor
/ FILE REFERENCE: MP12001-047P1RCP1(M)
/ CURRENT APPLICATION NUMBER: US/10/077,130
/ CURRENT FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: 60/259201
/ PRIOR FILING DATE: 2001-02-15
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 8106
/ TYPE: DNA
/ ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(71)
; NAME/KEY: CDS
; LOCATION: (72)...(7964)
; NAME/KEY: 3'UTR
; LOCATION: (7965)...(8106)
US-10-077-130-1

Query Match          94.9%; Score 4940.4; DB 14; Length 8106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4944; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 258 CCCAGGGCCCCCATCCATGAGTCAGGTAAACCATCGAGGATGTGCAGGCACACAGCAGCGCGAAC 3175
Db 3116 CGCAGCGCCCCCATCCATGAGTCAGGTAAACCATCGAGGATGTGCAGGCACACAGCAGCGCGAAC 3175

QY 318 GSCCCCAATTGAGGCTATCATTTAGGGGCGACCCACAGCCCTTCGGTGACCTCGGTACAAGGA 377
Db 3176 GSCCCCAATTGAGGCTATCATTTAGGGGCGACCCACAGCCCTTCGGTGACCTCGGTACAAGGA 3235

QY 378 CAGGCTCCAGCTGGTGACACGACACCCGGCTTAGCCAGCAGCAAGGACGACCATATCTC 437
Db 3236 CAGGCTCCAGCTGGTGACACGACACCCGGCTTAGCCAGCAGCAAGGACGACCATATCTC 3295

QY 438 CTTGGTGTGAGGCATGTGGCCCTCGAAGGATGCCGGCGCTTTACACCTCGCTCGGCCCAAAA 497

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Query Match 94.9%; Score 4940.4; DB 14; Length 8106;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4944; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

258	CCAGGGCCCCATCCATGAGGTATACCAATCGAGGATGTGACGACACAGACGCGGAAC	317	QY
3116	CGCAGGCCCCCATCCATGAGGTATACCAATCGAGGATGTGAGGCACACAGCGCGAAC	3175	Db
318	GGCCCAATTGAGGCTATCAATGAGGGGACCCACAGACCCCTCGGTGACCTGGTACAGGA	3177	QY
3176	GGCCCAATTGAGGCTATCAATGAGGGGACCCACAGACCCCTCGGTGACCTGGTACAGGA	3235	Db
378	GAGCGTCCAGCTGGTGACAGCACCCGGCTTATGCCAGAGACAGAGGCACCAATATCTC	437	QY
3236	CAGCGTCCAGCTGGTGACAGCACCCGGCTTATGCCAGAGCAAGAAGGCACCAATATCTC	3295	Db
438	CCTGGTGTGAGGCATGTGGCCCTCGAAGGATGCCGGCGCTTTACACCTTGCCTGGCGCCAAA	497	QY
3296	CCTGGTGTGAGGCATGTGGCCCTCGAAGGATGCCGGCGCTTTACACCTTGCCTGGCGCCAAA	3355	Db
498	CACCTGGTGGCCAGTGCTCTGCAAGGCAGAGCTGTGGTGTCTGGGGGGGACATGAGCC	557	QY
3356	CACCTGGTGGCCAGTGCTCTGCAAGGCAGAGCTGTGGTGTCTGGGGGGGACATGAGCC	3415	Db
558	GGACTCAGAGAAGCAAAAGCCACCGGAGGAAGTGCACCTCTTATGAGGTCAAGGAGGA	617	QY
3416	GGACTCAGAGAAGCAAAAGCCACCGGAGGAAGTGCACCTCTTATGAGGTCAAGGAGGA	3475	Db
618	GATTGGGAAGGGCGTGTTTGGCTTCGTAAAGAGTGCAGCACAAAGGAACACAGATCTT	677	QY
3476	GATTGGGAAGGGCGTGTTTGGCTTCGTAAAGAGTGCAGCACAAAGGAACACAGATCTT	3535	Db
678	GTGCGCTGCCAAGTTCAATCCCTACTCGAGACAGAACTCGGCGCCAGGCAATACAGGGAGCG	737	QY
3536	GTGCGCTGCCAAGTTCAATCCCTACTCGAGACAGAACTCGGCGCCAGGCAATACAGGGAGCG	3595	Db
738	AGACATCTGCGCGCGCTGAGCCACCGCTGGTCAACGGGGCTGTGGACACAGATTTGAGAC	797	QY
3596	AGACATCTGCGCGCGCTGAGCCACCGCTGGTCAACGGGGCTGTGGACACAGATTTGAGAC	3655	Db
798	CGGACAGACCTCATCTCATCTCGAGAGTGTGTCTCATCCGAGAGAGTGTGAGACGCGCT	857	QY
3656	CGGACAGACCTCATCTCATCTCGAGAGTGTGTCTCATCCGAGAGAGTGTGAGACGCGCT	3715	Db
858	GTACAGGAAGGGCGTGATGACGAGGCGCAGAGTCAAGGTCTACATCCAGCAGCTGTGTGGA	917	QY
3716	GTACAGGAAGGGCGTGATGACGAGGCGCAGAGTCAAGGTCTACATCCAGCAGCTGTGTGGA	3775	Db
918	GGGGCTGCATTAAGCTGCACAGCCATGGGGTCTCCACCTGACACATAAAGCCCTTAACAT	977	QY
3776	GGGGCTGCATTAAGCTGCACAGCCATGGGGTCTCCACCTGACACATAAAGCCCTTAACAT	3835	Db
978	CCTGATGGTGATCTCCCGCGGGAAGACATTAATAATCTGCGACTTTGGCTTTGCCCAGAA	1037	QY
3836	CCTGATGGTGATCTCCCGCGGGAAGACATTAATAATCTGCGACTTTGGCTTTGCCCAGAA	3895	Db
1038	CATCACCCGACGAGAGTCCAGTTCAGCCAGTAAAGGCTCCCGTCCCTGAGTTCGCTCCCGCA	1097	QY
3896	CATCACCCGACGAGAGTCCAGTTCAGCCAGTAAAGGCTCCCGTCCCGTCCCTGAGTTCGCTCCCGCA	3955	Db
1098	GATCATCCAGCAAAACCTGTGAGCGAAAGCCCTCCGACATTTGGGCCATGGGTGTCACTC	1157	QY
3956	GATCATCCAGCAAAACCTGTGAGCGAAAGCCCTCCGACATTTGGGCCATGGGTGTCACTC	4015	Db

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4458 GCTCCCTGCTGCTGGCGAGAGGGCTCCTACTCAGAACTCTGAGGTGAGAGACTACCTGTG 4511
7316 GCTCCCTGCTGCTGGCGAGAGGGCTCCTACTCAGAACTCGAGGTGAGAGACTACCTGTG 7375
4518 GCAGATGTTGAGTGGCCACCAGGACTCTGCHCAACAGAGCACTCTCGACCTGAGACTGAG 4577
7376 GCAGATGTTGAGTGGCCACCAGGACTCTGCHCAACAGAGCACTCTCGACCTGAGACTGAG 7435
4578 GTTCGAGAAATGATCATCACCGAATAACCTTGCTCAAGGTCTGCTGAGACTGGGCAATGC 4637
7436 GTTCGAGAAATGATCATCACCGAATAACCTTGCTCAAGGTCTGCTGAGACTGGGCAATGC 7495
4638 ACAGAGCTTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAAGGACTACCTAGAGAC 4697
7496 ACAGAGCTTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAAGGACTACCTAGAGAC 7555
4698 CATGCTTCCAGAGCTCCTCGAGGGCCAGGGGGGTGTTCACAGACAGACATCTGGGCCAT 4757
7556 CATGCTTCCAGAGCTCCTCGAGGGCCAGGGGGGTGTTCACAGACAGACATCTGGGCCAT 7615
4758 CGGTGTGACAGCTTCATCATCTGAGCGCGGAGTAGTACC CGGTGAGCAGCAGAGGTGCAG 4817
7616 CGGTGTGACAGCTTCATCATCTGAGCGCGGAGTAGTACC CGGTGAGCAGCAGAGGTGCAG 7675
4818 CGACTCTCAGAGAGGACTCCGCGAGGGGCTGTCCGGCTGAGCGCTGTCTACGCGGGCT 4877
7676 CGACTCTCAGAGAGGACTCCGCGAGGGGCTGTCCGGCTGAGCGCTGTCTACGCGGGCT 7735
4878 GTCGGGGGGCGCGTGGCTTCTGCGCAGCACTCTGTGGCCCGACAGCCCTGGGGCCGGCC 4937
7736 GTCGGGGGGCGCGTGGCTTCTGCGCAGCACTCTGTGGCCCGACAGCCCTGGGGCCGGCC 7795
4938 CTGCGCGTTCAGCTGCGCTCAGTGCCCTGTGCTTAACAGAGAGGGCCGCGCTGTTCGG 4997
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4998 GCCCGCGCCCTGACTTCCCTTACCGCGCGGCTGCGGCTTCTGTCGCAATCGCAGAA 5057
7856 GCCCGCGCCCTGACTTCCCTTACCGCGCGGCTGCGGCTTCTGTCGCAATCGCAGAA 7915
5058 GAGACGCGCTCTCTACAGAGCAACACTGGCCCAAGTGCCTGAGAGGTGCCCCCG 5117
7916 GAGACGCGCTCTCTACAGAGCAACACTGGCCCAAGTGCCTGAGAGGTGCCCCCG 7975
5118 GCCACACCTTGGCTTCCCGCTGGGGGTGCTGTCAGACGCGCCCAATAAAACGACAG 5177
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5178 CGGGCGAGAAAAA 5207
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RESULT 6
US-10-077-130-4
; Sequence 4, Application US/10077130
; Publication NO. US20020188742A1
GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; FILE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MF12001-047PRCPI (M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24120
; TYPE: DNA

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RESULT 5
US-10-077-130-4
// Sequence #, Application US/10077130
// Publication NO. US20020168742A1
// GENERAL INFORMATION:
// APPLICANT: Kapeller-Libermann, Rosana
// APPLICANT: Accon, Susan L.
// TITLE OF INVENTION: 59079 and 12599, Prot
// TITLE OF INVENTION: Members and Uses Ther
// FILE REFERENCES: MPI2001-047P/PCPI (M)
// CURRENT APPLICATION NUMBER: US/10/077,130
// CURRENT FILING DATE: 2002-03-15
// PRIOR APPLICATION NUMBER: 60/269201
// PRIOR FILING DATE: 2001-02-15
// NUMBER OF SEQ IDS: 9
// SOFTWARE: FastSeq for Windows version 4.0
// SEQ ID NO 4
// LENGTH: 24120
// TYPE: DNA

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[illegible]

ORGANISM: Homo sapiens
FEATURE: 5' UTR
NAME/KEY: (1)...(71)
LOCATION: CDS
NAME/KEY: CDS
LOCATION: (72)...(23978)
NAME/KEY: 3' UTR
LOCATION: (23979)...(24120)
US-10-077-130-4

Query Match 94.9%; Score 4940.4; DB 14; Length 24120;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4944; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	258	CCGAGGCCCCCATCCATGAGGTAAACCATCGAGGATGTGCAGGCACACAGAGCGGGAAC	317
Db	19130	CGCAGCGCCCCCATCCATGAGGTAAACCATCGAGGATGTGCAGGCACACAGAGCGGGAAC	19189
Qy	318	GGCCCAATTCAGAGCTATCATTTAGGCGCACCCACAGCCCTCGTGACCTGTGTACAAGGA	377
Db	19190	GGCCCAATTCAGAGCTATCATTTAGGCGCGACCCACAGCCCTCGGTGACCTGTGTACAAGGA	19249
Qy	378	CAGCGTCCAGCTGTGACAGCAGCCCGCTTACCCAGCAGCAGAGGACACACATATCTC	437
Db	19250	CAGCGTCCAGCTGTGACAGCAGCCCGCTTACCCAGCAGCAGAGGACACACATATCTC	19309
Qy	438	CTGSGTCTGAGGCATGTGCGCTCGAAGGATGCGCGCTTTACAACCTGCTGCGCCAAA	497
Db	19310	CCTGSGTCTGAGGCATGTGCGCTCGAAGGATGCGCGCTTTACAACCTGCTGCGCCAAA	19369
Qy	498	CACGTGCGCCAGGTCTCTGCAAGGCAGAGCTGCTGCTGCTGCGGCGGACAAATGAGCC	557
Db	19370	CACGTGCGCCAGGTCTCTGCAAGGCAGAGCTGCTGCTGCTGCGGCGGACAAATGAGCC	19429
Qy	558	GGATCAGAGAGCAAAAGCCACCGGAGGAAGCTGCACTCTTCTATGAGGTCAAGGAGGA	617
Db	19430	GGATCAGAGAGCAAAAGCCACCGGAGGAAGCTGCACTCTTCTATGAGGTCAAGGAGGA	19489
Qy	618	GATTGGAAGGGCGTGTGGCTTCGTAAGAGAGTGCAGCACAAGGAAACAAGATCTT	677
Db	19490	GATTGGAAGGGCGTGTGGCTTCGTAAGAGAGTGCAGCACAAGGAAACAAGATCTT	19549
Qy	678	GTGCGTCCCAAGTTATCCCTTACGAGCAGAACTCGGCGCCAGGCATACAGGAGCG	737
Db	19550	GTGCGTCCCAAGTTATCCCTTACGAGCAGAACTCGGCGCCAGGCATACAGGAGCG	19609
Qy	738	AGACATCTGCGCGCTGAGCCACCGCTGGTCAAGGAGCTGCTGAGCCAGCTTTGAGAC	797
Db	19610	AGACATCTGCGCGCTGAGCCACCGCTGGTCAAGGAGCTGCTGAGCCAGCTTTGAGAC	19669
Qy	798	CCGCAAGACCTCATCTCTCATCTGAGCTGTGCTCATCCGAGGAGCTGCTGGAACCGCT	857
Db	19670	CCGCAAGACCTCATCTCTCATCTGAGCTGTGCTCATCCGAGGAGCTGCTGGAACCGCT	19729
Qy	858	GTCAGGAGGGCTGTGACGAGCCGAGGTCAGAGTCAAGGTCATCCAGCAGCTGTGGA	917
Db	19730	GTCAGGAGGGCTGTGACGAGCCGAGGTCAGAGTCAAGGTCATCCAGCAGCTGTGGA	19789
Qy	918	GGGCTGCACCTACCTGCACAGCCATGGCGTTCTCCAACCTGGAATAAAGCCCTTAAACAT	977
Db	19790	GGGCTGCACCTACCTGCACAGCCATGGCGTTCTCCAACCTGGAATAAAGCCCTTAAACAT	19849
Qy	978	CCTGATGTCATCTCTCCCGGAGAGCATTAATTCGCACTTGGCTTTGGCCAGAA	1037
Db	19850	CCTGATGTCATCTCTCCCGGAGAGCATTAATTCGCACTTGGCTTTGGCCAGAA	19909
Qy	1038	CATCACCACAGCAGAGCTGAGTTCAGCCAGTACGCTCCCTCGATGCTGCTCCCCCGA	1097
Db	19910	CATCACCACAGCAGAGCTGAGTTCAGCCAGTACGCTCCCTCGATGCTGCTCCCCCGA	19969
Qy	1098	GATCATCCAGCAGACCTGTGAGCAGAGCTCCGACATTTGGCCATGGGTGTGATCTC	1157
Db	19970	GATCATCCAGCAGACCTGTGAGCAGAGCTCCGACATTTGGCCATGGGTGTGATCTC	20029

Qy	1158	CTACCTCAGCCTGACCTGCTCATCCCATTTTCCGCGAGAGTACCTGCGCACCCCTCTCT	1217
Db	20030	CTACCTCAGCCTGACCTGCTCATCCCATTTTCCGCGAGAGTACCTGCGCACCCCTCTCT	20089
Qy	1218	GAACGTCCTGGAGGGCGGCTGTCATGGAGAGCCCATGGCTGCCACCTCAGCGRAGA	1277
Db	20090	GAACGTCCTGGAGGGCGGCTGTCATGGAGAGCCCATGGCTGCCACCTCAGCGRAGA	20149
Qy	1278	CGCAAGAAGCTTCAATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGCTAGTGCGC	1337
Db	20150	CGCAAGAAGCTTCAATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGCTAGTGCGC	20209
Qy	1338	CCAGTGCCTCTCCCAACCCCTGGTTCTGAAATCCATGCTCGGAGAGGAGCCCACTTCAT	1397
Db	20210	CCAGTGCCTCTCCCAACCCCTGGTTCTGAAATCCATGCTCGGAGAGGAGCCCACTTCAT	20269
Qy	1398	CAACACAAAGAGCTCAAGTTCTCTGCCCCCAAGTGCCTGCGAGAGCTTCCCTGATGAG	1457
Db	20270	CAACACAAAGAGCTCAAGTTCTCTGCCCCCAAGTGCCTGCGAGAGCTTCCCTGATGAG	20329
Qy	1458	CTAACAAGTCCATCTCTGATGCTGCTCATCCCTGAGTGTGCGGGGCCACCCGACAG	1517
Db	20330	CTAACAAGTCCATCTCTGATGCTGCTCATCCCTGAGTGTGCGGGGCCACCCGACAG	20389
Qy	1518	CCCTCTCCCTGCGGTAGCCCGGCACTCTGCAAGGACACTGCTGCTGCTCTCCAGTTCCTC	1577
Db	20390	CCCTCTCCCTGCGGTAGCCCGGCACTCTGCAAGGACACTGCTGCTGCTCTCCAGTTCCTC	20449
Qy	1578	CTCTCTCTCTGACAAAGAGCTGCGCCCATTTTCCGCGGCTAAGTCACTGCGCACCCCTCCC	1637
Db	20450	CTCTCTCTCTGACAAAGAGCTGCGCCCATTTTCCGCGGCTAAGTCACTGCGCACCCCTCCC	20509
Qy	1638	GCTGACACACTACCACTGCTGCAACCCCGGGGCTTCTGCGGCTCTGCGCCAGCTGCTC	1697
Db	20510	GCTGACACACTACCACTGCTGCAACCCCGGGGCTTCTGCGGCTCTGCGCCAGCTGCTC	20569
Qy	1698	TGAGGAAGCCGAGGCGCAGTGAGCGCTCCACCGAGGCCCCAGCTCCGCTGCTCATCTCCGA	1757
Db	20570	TGAGGAAGCCGAGGCGCAGTGAGCGCTCCACCGAGGCCCCAGCTCCGCTGCTCATCTCCGA	20629
Qy	1758	GGTGTCCGCGGACACCGCGCCGAGGCTGCTGCGCCCGGACAGCTGCTCAGAGCTC	1817
Db	20630	GGTGTCCGCGGACACCGCGCCGAGGCTGCTGCGCCCGGACAGCTGCTCAGAGCTC	20689
Qy	1818	GTCTTACCACAGGCGGTGAGAGCCCTGAGCACGGGGCCCTGCGCCCGGGGAGCAGGCG	1877
Db	20690	GTCTTACCACAGGCGGTGAGAGCCCTGAGCACGGGGCCCTGCGCCCGGGGAGCAGGCG	20749
Qy	1878	GCACCGCGCCCGCGCGGCGACCTGCTGAAAGGCGGCTACATTCGCGGGGCGCTGCCAGG	1937
Db	20750	GCACCGCGCCCGCGCGGCGACCTGCTGAAAGGCGGCTACATTCGCGGGGCGCTGCCAGG	20809
Qy	1938	CCTGCGCAGCCACTGATGGAGCACCGGCTGCTGAGAGGAGGCGCGCCAGGAGGAGCA	1997
Db	20810	CCTGCGCAGCCACTGATGGAGCACCGGCTGCTGAGAGGAGGCGCGCCAGGAGGAGCA	20869
Qy	1998	GGCCACCTCTGCGCAAGAGCCCTCATTTGAGACTGCTGCTGCGGCTGCTGCTGCTG	2057
Db	20870	GGCCACCTCTGCGCAAGAGCCCTCATTTGAGACTGCTGCTGCGGCTGCTGCTGCTG	20829
Qy	2058	CACCCACTTTGGCCCTCGGCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCGCG	2117
Db	20930	CACCCACTTTGGCCCTCGGCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCGCG	20989
Qy	2118	CCCTCTCTGAGAGGCTGCGGTGAGGACACAGGACTGCTTTCAGCCCTCCCGGGGGGGC	2177
Db	20990	CCCTCTCTGAGAGGCTGCGGTGAGGACACAGGACTGCTTTCAGCCCTCCCGGGGGGGC	21049
Qy	2178	CCCTATCAGGAGACATGGGGCACCCCTCAGGGCTCCAAAGCAGCTTCCATCCAGTGGCCA	2237
Db	21050	CCCTATCAGGAGACATGGGGCACCCCTCAGGGCTCCAAAGCAGCTTCCATCCAGTGGCCA	21109

Qy	2238	CCCAGGCACTGCTCTCAGCCAGAGAGGGCCATCCCCGGACAGCCCTTGGGGGACGCCAGCAGCC	2297
Db	21110	CCCAGGCACTGCTCTCAGCCAGAGAGGGCCATCCCCGGACAGCCCTTGGGGGACGCCAGCAGCC	21169
Qy	2298	TTTCTGCAACCCAAAGCAGGGTCTGTCGCCCCACAGGAGGGTCGAGCCCCACCCAGCAGT	2357
Db	21170	TTTCTGCCACCCCAAGCAGGGTCTGTCGCCCCACAGGAGGGTCGAGCCCCACCCAGCAGT	21229
Qy	2358	TGCCCATGCCCTCTGCTCTCTTCCCTCTCAGGATCTTGGCAAAGAGGCCCTCTTAGTACC	2417
Db	21230	TGCCCATGCCCTCTGCTCTCTTCCCTCTCAGGATCTTGGCAAAGAGGGCCCTCTTAGTACC	21289
Qy	2418	CTCAAGCCCTTCTTTGGGACAGCCCAAGGACACCCCTGCCCTTGCCCAAAGCAAGCCGCC	2477
Db	21290	CTCAAGCCCTTCTTTGGGACAGCCCAAGGACACCCCTGCCCTTGCCCAAAGCAAGCCGCC	21349
Qy	2478	ATTGGACTTAAAGTGGGGCTGGAGACATCTCTCTTCTGGGAGGCCAAACCCGGGCC	2537
Db	21350	ATTGGACTTAAAGTGGGGCTGGAGACATCTCTCTTCTGGGAGGCCAAACCCGGGCC	21409
Qy	2538	CTCAGTTCCCAAGGTCAGCCTCCAGCGAGCTCTTCCCAAGTAGCTCCCTCAGGGT	2597
Db	21410	CTCAGTTCCCAAGGTCAGCCTCCAGCGAGCTCTTCCCAAGTAGCTCTCCCTCAGGGT	21469
Qy	2598	GGGCTCTCCAGGTGGGCACAGAGCTTGGCCCTCCCTGGATGGGAGGGCTGACCCA	2657
Db	21470	GGGCTCTCCAGGTGGGCACAGAGCTTGGCCCTCCCTGGATGGGAGGGCTGACCCA	21529
Qy	2658	GGAGGCTGAGATCTGTCCGACTCCAACCCACTTGCAGCGGCTCAGGAACAGGTGAC	2717
Db	21530	GGAGGCTGAGATCTGTCCGACTCCAACCCACTTGCAGCGGCTCAGGAACAGGTGAC	21589
Qy	2718	CATGCGCAAGTCTCTCCTGGTGGTCGCGGGGCTACGCAGAGCTGGCTGGGTATGGCAC	2777
Db	21590	CATGCGCAAGTCTCTCCTGGTGGTCGCGGGGCTACGCAGAGCTGGCTGGGTATGGCAC	21649
Qy	2778	CTTTGCTTTTGTGTGAGATGCAAGGGGCAATCTTGGGGCAGGGGCCCATGTGGGCCAGGAT	2837
Db	21650	CTTTGCTTTTGTGTGAGATGCAAGGGGCAATCTTGGGGCAGGGGCCCATGTGGGCCAGGAT	21709
Qy	2838	AGCCTGGGCTGTGTCCTCAGTCGGAGAGGAGGACGAGGAGGCGCAGGCTGAGTCCCA	2897
Db	21710	AGCCTGGGCTGTGTCCTCAGTCGGAGAGGAGGACGAGGAGGCGCAGGCTGAGTCCCA	21769
Qy	2898	GTGGAGGACACGACGAGGCGCAGGGCTGAGAGCCCATCTGCCCAAGTCAGTGCAAGGCC	2957
Db	21770	GTGGAGGACACGACGAGGCGCAGGGCTGAGAGCCCATCTGCCCAAGTCAGTGCAAGGCC	21829
Qy	2958	TGTGCTTAGGTCGGCAGGGCTCCCAACAGGAGCTCTCCAGAGGCCACCCCATGGGAGGA	3017
Db	21830	TGTGCTTAGGTCGGCAGGGCTCCCAACAGGAGCTCTCCAGAGGCCACCCCATGGGAGGA	21889
Qy	3018	CATCGGGCAGGTCCTCCCTGGTGCAGATCCGGACCTGTGAGTGTGCGAGGCGGCCGA	3077
Db	21890	CATCGGGCAGGTCCTCCCTGGTGCAGATCCGGACCTGTGAGTGTGCGAGGCGGCCGA	21949
Qy	3078	CACAATATCCCTGGACATTTCCGAGGTGACCCCGCCCTACCTCAACCTCTCAGACCTGTA	3137
Db	21950	CACAATATCCCTGGACATTTCCGAGGTGACCCCGCCCTACCTCAACCTCTCAGACCTGTA	22009
Qy	3138	CGATATCAAGTACTCCCATTCGAGTTTATGATCTTCAGGAAGTCCCGAGTCGGCTCA	3197
Db	22010	CGATATCAAGTACTCCCATTCGAGTTTATGATCTTCAGGAAGTCCCGAGTCGGCTCA	22069
Qy	3198	GCCAGAGCGCCCTCCCCCATGGCTGAGGAGGAGTGGCCGAGTTTCCCGGAGCCACGTG	3257
Db	22070	GCCAGAGCGCCCTCCCCCATGGCTGAGGAGGAGTGGCCGAGTTTCCCGGAGCCACGTG	22129
Qy	3258	GCCCTGGCAGGTGACTGGGCCCCACGACAGGCTGGATTCACAGAGGAGTCAAGGA	3317
Db	22130	GCCCTGGCAGGTGACTGGGCCCCACGACAGGCTGGATTCACAGAGGAGTCAAGGA	22189
Qy	3318	TGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAAGGCAAGTGGTCTCTCGCGTC	3377

Db	22190	TGTGGACCGCGCTGCTGGCAGAGGCTGCCGTGGGAGGAAGCGCAAGTGGTCTCTCGCGCTC	22249
Qy	3378	ACGCAGCGCTCTCCACTTCCCTGGGAGGACACTGCCCTGGATGAGCTGTCGAGAGCTGGG	3437
Db	22250	ACGCAGCGCTCTTCCACTTTCCTTGGGAGGACCTGCCGCTGATGAGCCTCGAGAGCTGGG	22309
Qy	3438	GCTCGGTGAGAGAGTGAAAGGCTTCGTTGGAGACACTTCCCGGATCTCTGAAGGCGACGCC	3497
Db	22310	GCTCGGTGAGAGAGTGAAAGGCTTCGTTGGAGACACTTCCCGGATCTCTGAAGGCGACGCC	22369
Qy	3498	GGAAAGTCTGGAGAGAGGGGGCCCCCAGGAAGAGCAGGCGCTTGCTTCTCTCCGGCT	3557
Db	22370	GGAAAGTCTGGAGAGAGGGGGCCCCCAGGAAGAGCAGGCGCTTGCTTCTCTCCGGCT	22429
Qy	3558	CTCAGGTCTGAAGAGCTGGGACGAGAGCGCGGACATTCTTAAGGAGCTCTCAGATGAGAC	3617
Db	22430	CTCAGGTCTGAAGAGCTGGGACGAGAGCGCGGACATTCTTAAGGAGCTCTCAGATGAGAC	22489
Qy	3618	TGTGGTCTTGGGCGAGTCAAGTGACACTGGCTTGCCAGGTGTGAGCCAGCAGCTGCCCA	3677
Db	22490	TGTGGTCTTGGGCGAGTCAAGTGACACTGGCTTGCCAGGTGTGAGCCAGCAGCTGCCCA	22549
Qy	3678	GGCCACTGGAGCAAGACGGAGCGCCCTTGGAGAGCAGACCGTGTCTCATCTCTGC	3737
Db	22550	GGCCACTGGAGCAAGACGGAGCGCCCTTGGAGAGCAGACCGTGTCTCATCTCTGC	22609
Qy	3738	CACCCTCAAGAACTTCCAGCTTCTGACCATTCTGTGGTGTGGCTGAGGACCTGGGTGT	3797
Db	22610	CACCCTCAAGAACTTCCAGCTTCTGACCATTCTGTGGTGTGGCTGAGGACCTGGGTGT	22669
Qy	3798	GTACACCTTCAGCGTGAGCAATGGCCTGGGACACAGTGACACACAGGCGCTCTCTCCGGA	3857
Db	22670	GTACACCTTCAGCGTGAGCAATGGCCTGGGACACAGTGACACACAGGCGCTCTCTCCGGA	22729
Qy	3858	GGCAGAGCGCCCTCATCTTCCCATGCCCAGATATCGGGAGGTGTACCGGATGGGT	3917
Db	22730	GGCAGAGCGCCCTCATCTTCCCATGCCCAGATATCGGGAGGTGTACCGGATGGGT	22789
Qy	3918	GCTGCTGCTGTGAAGCGCGTGGAAATCTAGCGCCCTGTGACCTPACATTGTGCAGTGCAG	3977
Db	22790	GCTGCTGCTGTGAAGCGCGTGGAAATCTAAGCGCCCTGTGACCTACATTGTGAGTGCAG	22849
Qy	3978	CTTAGAAGCGGAGCTGGACACACTGGCTTCGACATCTTTGACTGCTGCTACTGTAC	4037
Db	22850	CCTAGAAGCGGAGCTGGACACACTGGCTTCGACATCTTTGACTGCTGCTACTGTAC	22909
Qy	4038	CAGCAAGCTCTCCGGGGTGGACCTACACTTTCGACGCGCATGTGTCAAGCAAGGCAGG	4097
Db	22910	CAGCAAGCTCTCCGGGGTGGACCTACACTTTCGACGCGCATGTGTCAAGCAAGGCAGG	22969
Qy	4098	AATGGTTCGTTACAGGAGCCCTCGGACAGTCTCTCTGGAGGGGCCAGGACCTTGGC	4157
Db	22970	AATGGTTCGTTACAGGAGCCCTCGGACAGTCTCTCTGGAGGGGCCAGGACCTTGGC	23029
Qy	4158	CTCTGAGGAGGAGCCAGGGGCGGTGAGCCCAACCCCTGCCAGCACAAAGACCTTCGC	4217
Db	23030	CTCTGAGGAGGAGCCAGGGGCGGTGAGCCCAACCCCTGCCAGCACAAAGACCTTCGC	23089
Qy	4218	ATTTCAGACACAGATCCAGAGGGCGGCTTCAGCGTGGTGGCGCATGTCTGGAGAGGC	4277
Db	23090	ATTTCAGACACAGATCCAGAGGGCGGCTTCAGCGTGGTGGCGCATGTCTGGAGAGGC	23149
Qy	4278	CAGCGGCGGGCGCTGGCGCCAGATCATCCCCCTACCCCAAGGACAAAGACAGT	4337
Db	23150	CAGCGGCGGGCGCTGGCGCCAGATCATCCCCCTACCCCAAGGACAAAGACAGT	23209
Qy	4338	GCTGCGCGAATACAGAGGCCCTCAAGGGGCTGGGCCACCCGACCTGGCCCGAGTCACGC	4397
Db	23210	GCTGCGCGAATACAGAGGCCCTCAAGGGGCTGGGCCACCCGACCTGGCCCGAGTCACGC	23269
Qy	4398	AGCCTACTCAGCGCCCGGACACTGGTGCTCATCTTGGAGCTGTGCTTGGGCGCGAGT	4457


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Db 23270 AGCTACTCTCAGCCCCCGGACCTGGTGTCTCATTTGGAGCTGTCTCTGGGCCCGAGCT 23329
Qy 4458 GTCCTCTGCTGCTGCCGAGAGGCTCTCTACTCAGAACTCTGAGGTGAAGACTACTCTGTG 4517
Db 23330 GCTCTCTGCTGCTGCCGAGAGGCTCTCTACTCAGAACTCTGAGGTGAAGACTACTCTGTG 23389
Qy 4518 GCAGATTTGAGTGCCACCCAGTACTCTGCACAAACAGACATCTCTGCACCTTGAGACTGAG 4577
Db 23390 GCAGATTTGAGTGCCACCCAGTACTCTGCACAAACAGACATCTCTGCACCTTGAGACTGAG 23449
Qy 4578 GTCCGAGAAATGATCATATCAACCAATACAACTGCTCAAGGTCTGGAGACTCTGGGCAATGC 4637
Db 23450 GTCCGAGAAATGATCATATCAACCAATACAACTGCTCAAGGTCTGGAGACTCTGGGCAATGC 23509
Qy 4638 ACAGAGCTCTGAGCAGAGAGAGTGTCTGCTCAGCAAAAGTTCAAAGACTACTCTAGAGAC 4697
Db 23510 ACAGAGCTCTGAGCAGAGAGAGTGTCTGCTCAGCAAAAGTTCAAAGACTACTCTAGAGAC 23569
Qy 4698 CATGGCTTCCAGAGCTCTGAGAGGCTCAGAGGCTGTCTCAGACAGACATCTGGGCCAT 4757
Db 23570 CATGGCTTCCAGAGCTCTGAGAGGCTCAGAGGCTGTCTCAGACAGACATCTGGGCCAT 23629
Qy 4758 CGGTGTGACAGCTCTCATCTGAGAGGCTCAGAGGCTGTCTCAGACAGACATCTGGGCCAT 4817
Db 23630 CGGTGTGACAGCTCTCATCTGAGAGGCTCAGAGGCTGTCTCAGACAGACATCTGGGCCAT 23689
Qy 4818 CGACCTGCAGAGAGGCTCTGCGCAAGGGCTGTCTCGGCTGAGCCGCTGTCTACGCGGGGCT 4877
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Qy 4878 GTCCGGGGGCGCGTGGCTCTCTGCGAGGCTCTGTGCGGCTGAGCCGCTGTGCGGGCGGCC 4937
Db 23750 GTCCGGGGGCGCGTGGCTCTCTGCGAGGCTCTGTGCGGCTGAGCCGCTGTGCGGGCGGCC 23809
Qy 4938 CTGCGCTGCTCAGCTGCTGCTGAGTGGCTGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTG 4997
Db 23810 CTGCGCTGCTCAGCTGCTGCTGAGTGGCTGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTG 23869
Qy 4998 GCGCGGCGCGTGAACCTTCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 5057
Db 23870 GCGCGGCGCGTGAACCTTCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 23929
Qy 5058 GAGACGCGCGCTGCTGTACAGAGGACAACTGCGGCTGAGGCTGCTGAGGCTGCTGCGCCCG 5117
Db 23930 GAGACGCGCGCTGCTGTACAGAGGACAACTGCGGCTGAGGCTGCTGAGGCTGCTGCGCCCG 23989
Qy 5118 GCGACACCTTGTCTCTCCGCTGCGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTG 5177
Db 23990 GCGACACCTTGTCTCTCCGCTGCGGCTGCTGCTGCGGCTGCTGCTGCGGCTGCTGCTGCTG 24049
Qy 5178 CGGCGGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 5207
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RESULT 7

US-10-307-019-3

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; Sequence 3, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DV1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 3
; LENGTH: 5007
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)...(4926)
US-10-307-019-3
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Query Match 94.4%; Score 4915.8; DB 15; Length 5007;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4920; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 258 CCCAGGCCCCCATCTCATCTGAGGTAAACCATCGAGGATGTGAGGACACAGACAGCGGGAAC 317
Db 81 CGCAGGCCCCCATCTCATCTGAGGTAAACCATCGAGGATGTGAGGACACAGACAGCGGGAAC 140
Qy 318 GGCACCAATTCGAGGCTATCATTTAGGGGAGCCACAGCCCTCGGTGACCTGTGTAACAGGA 377
Db 141 GGCACCAATTCGAGGCTATCATTTAGGGGAGCCACAGCCCTCGGTGACCTGTGTAACAGGA 200
Qy 378 CAGCGTCCAGCTGTGTGGAGCAGACCCCGCTTAGCCAGCAGCAAGAGCCACCATACTC 437
Db 201 CAGCGTCCAGCTGTGTGGAGCAGACCCCGCTTAGCCAGCAGCAAGAGCCACCATACTC 260
Qy 438 CTTGTGTCTGAGGCAATGTGGCTCTGAAAGATCCCGGCTTTACACCTGCTCGGCCCAAAA 497
Db 261 CTTGTGTCTGAGGCAATGTGGCTCTGAAAGATCCCGGCTTTACACCTGCTCGGCCCAAAA 320
Qy 498 CACTGTGCGGCGAGTGTCTGGAAGGAGAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 557
Db 321 CACTGTGCGGCGAGTGTCTGGAAGGAGAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 380
Qy 558 GGACTCAGAGAGCAAAAGCCACCGAGAGGAGCTGCACTCTCTTATGAGGTCAAGGAGGA 617
Db 381 GGACTCAGAGAGCAAAAGCCACCGAGAGGAGCTGCACTCTCTTATGAGGTCAAGGAGGA 440
Qy 618 GATTGGAAGGGCGTGTGTGGCTTCTGTAAGAAGTGCAGCAAAAGGAAACAAGATCTT 677
Db 441 GATTGGAAGGGCGTGTGTGGCTTCTGTAAGAAGTGCAGCAAAAGGAAACAAGATCTT 500
Qy 678 GTGCGCTGCGCAAGTTCATCCCTTACCGAGCAGAACTCGGGGCCCGAGCATAACAGGAGCG 737
Db 501 GTGCGCTGCGCAAGTTCATCCCTTACCGAGCAGAACTCGGGGCCCGAGCATAACAGGAGCG 560
Qy 738 AGACATCTGCGCGCGCTGAGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Db 561 AGACATCTGCGCGCGCTGAGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Qy 798 CCGCAAGACCTCTCATCTCTGAGCTGTGCTCATCCGAGGAGCTGTGAGACCGCCT 857
Db 621 CCGCAAGACCTCTCATCTCTGAGCTGTGCTCATCCGAGGAGCTGTGAGACCGCCT 680
Qy 858 GTACAGGAAGGGCTGTGAGGAGGCGGAGGTCAAGGTCTACATCCAGCAGCTGTGGA 917
Db 681 GTACAGGAAGGGCTGTGAGGAGGCGGAGGTCAAGGTCTACATCCAGCAGCTGTGGA 740
Qy 918 GGGGCTGCACCTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTTAACAT 977
Db 741 GGGGCTGCACCTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTTAACAT 800
Qy 978 CCGTGTGTGTGATCTCTGCGGAGAGCATTAAATCTGCGATTGCTGCTGCTGCTGCTGCTGCTG 1037
Db 801 CCGTGTGTGTGATCTCTGCGGAGAGCATTAAATCTGCGATTGCTGCTGCTGCTGCTGCTGCTG 860
Qy 1038 CATCACCCCGCAGCAGCTGTGAGTTTCAAGGCTAGGCTCCCTCTGAGTTCTCTCTCCCGGA 1097
Db 861 CATCACCCCGCAGCAGCTGTGAGTTTCAAGGCTAGGCTCCCTCTGAGTTCTCTCTCCCGGA 920
Qy 1098 GATCATCCAGCAGAACCTGTGAGGAGGCTCGGACATTTGGGCCCATGGGTGTCTATCTC 1157
Db 921 GATCATCCAGCAGAACCTGTGAGGAGGCTCGGACATTTGGGCCCATGGGTGTCTATCTC 980
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1158 CTACCTCAGCCTGACCTGCTCATCCCATTTGCGGAGAGTGACCGTGCCACCTCCT 1217
Db
981 CTACCTCAGCCTGACCTGCTCATCCCATTTGCGGAGAGTGACCGTGCCACCTCCT 1040
Qy
1218 GAACGCTCTGGAGGGGCGGTGTATGAGAGAGCCCATATGCTGCCCCCATCTCAGCGAAGA 1277
Db
1041 GAACGCTCTGGAGGGGCGGTGTATGAGAGAGCCCATATGCTGCCCCCATCTCAGCGAAGA 1100
Qy
1278 CGCAAAAGACTTCAACAAGGCTACGCTGCAGAGAGCCCTCAGGCGCGGCTAGTGCAGC 1337
Db
1101 CGCAAAAGACTTCAACAAGGCTACGCTGCAGAGAGCCCTCAGGCGCGGCTAGTGCAGC 1160
Qy
1338 CCAAGTGCCTCTCCACCCCTGGTTCTGAAATCCATGCTGCGGAGAGAGCCCATTTCA 1397
Db
1161 CCAAGTGCCTCTCCACCCCTGGTTCTGAAATCCATGCTGCGGAGAGAGCCCATTTCA 1220
Qy
1398 CACACCAAGAGCTCAAGTTCTCTGCGCCGAGTCCGCTGCAGGCTTCCCTGATGAG 1457
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1221 CAACCAAGAGCTCAAGTTCTCTGCGCCGAGTCCGCTGCAGGCTTCCCTGATGAG 1280
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1458 CTACAAGTCCATCTGCTGATGCTCCATCTGAGCTGCTGCGGGGCCACCCGACAG 1517
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1281 CTACAAGTCCATCTGCTGATGCTCCATCTGAGCTGCTGCGGGGCCACCCGACAG 1340
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1518 CCCTCTCCTGGGCTAGCCCGGACCTCTGACGGGACATGCTGGCTCTCCAGATTCCTC 1577
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1341 CCCTCTCCTGGGCTAGCCCGGACCTCTGACGGGACATGCTGGCTCTCCAGATTCCTC 1400
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1578 CTCCTCTCTGACAAAGAGCTGCGCCCATTTGCGGGCTAAAGTCACTGCACTCCCTCCC 1637
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1401 CTCCTCTCTGACAAAGAGCTGCGCCCATTTGCGGGCTAAAGTCACTGCACTCCCTCCC 1460
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1638 GGTGACACATCACTGCTGACACCCCGGGCTTCTGCGGCTCTGCGGACGCTGCG 1697
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1938 CTTGCGGAGCCTGATGAGGACCGGCTGCTGAGGAGGAGGCGCCGAGGAGGAGCA 1997
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1761 CTTGCGGAGCCTGATGAGGACCGGCTGCTGAGGAGGAGGCGCCGAGGAGGAGCA 1820
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1998 GGCCACCTCTCTGCGGCAAGCCCTCATTCGAGACTGCGCTCGGCTGCTGCTGCTG 2057
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3021 GCCAGAGCGGCTCCCGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAG 3080
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3258 GCGCTTGGCGAGGCTAACTGGGCGCCCGCAGCGAGGCTGGAGATCAAGAGGAGTCAAG 3317
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3081 GCGCTTGGCGAGGCTAACTGGGCGCCCGCAGCGAGGCTGGAGATCAAGAGGAGTCAAG 3140
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3318 TGTGAGCGGCTGCTGCGAGGCTGCGTGGGCAAGGCTGCGTGGGCAAGGCTGCTGCTG 3377

4458	QY	GCTCCCTGCTGCGCGAGAGGGCTCCTACTCAGAACTGAGGTGAAGCACTACCTGTG	45117
4281	Db	GCTCCCTGCTGCGCGAGAGGGCTTCTACTAGAACTCGAGGTGAAGCACTACCTGTG	43400
4518	QY	GCAGATGTTGAGTGCACCCAGTACTGCAACAACGACATCTCTGCACTTGACCTGAG	4577
4341	Db	GCAGATGTTGAGTGCACCCAGTACTGCAACAACGACATCTCTGCACTTGACCTGAG	4400
4578	QY	GTCGAGAACATGATCATCACCGATACAACTGCTCAAGTCTGAGGCTGCGCAATGC	4637
4401	Db	GTCGAGAACATGATCATCACCGATACAACTGCTCAAGTCTGAGGCTGCGCAATGC	4460
4638	QY	ACAGAGCTTCAGCCAGGAAAGTGTGTCCTCAGACAAAGTTCAAAGGACTACTAGAGAC	4697
4461	Db	ACAGAGCTTCAGCCAGGAAAGTGTGTCCTCAGACAAAGTTCAAAGGACTACTAGAGAC	4520
4698	QY	CATGGTTCAGAGCTCTCGAGGGCCAGGGGGCTGTTCCACAGACAGACATCTGGGGCCAT	4757
4521	Db	CATGGTTCAGAGCTCTCGAGGGCCAGGGGGCTGTTCCACAGACAGACATCTGGGGCCAT	4580
4758	QY	CGGTGTGACAGCCTTCATCATGCTGAGCGCCAGTACC CGGTGAGCAGGAGGGTGCACG	4817
4581	Db	CGGTGTGACAGCCTTCATCATGCTGAGCGCCAGTACC CGGTGAGCAGGAGGGTGCACG	4640
4818	QY	CGACCTGCAGAGAGGACTGCGCAAGGGGTGGTCCGGCTGAGCGCTGTCTACCGGGGCT	4877
4641	Db	CGACCTGCAGAGAGGACTGCGCAAGGGGTGGTCCGGCTGAGCGCTGTCTACCGGGGCT	4700
4878	QY	GTCCGGGGGCGCGTGGCCTTCCTGTCGCGACACTCTGTGCGCCACGCCCTGGGGCGCGCC	4937
4701	Db	GTCCGGGGGCGCGTGGCCTTCCTGTCGCGACACTCTGTGCGCCACGCCCTGGGGCGCGCC	4760
4938	QY	CTCGCGCTGCAGTGTGCTGCAGTGCCCGTGGCTTAAACAGAGGAGGGCCCGGCTGTTCGCG	4997
4761	Db	CTCGCGCTGCAGTGTGCTGCAGTGCCCGTGGCTTAAACAGAGGAGGGCCCGGCTGTTCGCG	4820
4998	QY	GCCCGCGCCCGTGACCTTCCCTACCGGGGGCTGCGCGCTCTGCTGGGCAATCGCGAGAA	5057
4821	Db	GCCCGCGCCCGTGACCTTCCCTACCGGGGGCTGCGCGCTCTGCTGGGCAATCGCGAGAA	4880
5058	QY	GAGACGCGCGCTGCTGTACAAAGAGGACAACTTGGGCCCAAGGTGCGGTGAGGGTTCGCCCG	5117
4881	Db	GAGACGCGCGCTGCTGTACAAAGAGGACAACTTGGGCCCAAGGTGCGGTGAGGGTTCGCCCG	4940
5118	QY	GCCACACCTTGGTCTCCCGCTGGGGGTGCTGTGACAGCGCGCAATATAAAGCGCACAGC	5177
4941	Db	GCCACACCTTGGTCTCCCGCTGGGGGTGCTGTGACAGCGCGCAATATAAAGCGCACAGC	5000
5178	QY	CGGGCGA 5184	
5001	Db	CGGGCGA 5007	

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RESULT 8
US-10-307-019-5
; Sequence 5, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021dV1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

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LENGTH: 7928
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (60)...(7847)
US-10-019-5

Query Match. 94.4%; Score 4915.8; DB 15; Length 7928;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4920; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	258	CCGAGGCCCCCATCATGAGGTAAACCATCGAGGATGACAGGACACAGACAGGCGGAAC	317
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QY	318	GGCCCAATTCGAGGCTATCATTTAGGGGACACACAGCCCTCGGTGACCTGGTCAAGGA	377
DB	3062	GGCCCAATTCGAGGCTATCATTTAGGGGACACACAGCCCTCGGTGACCTGGTCAAGGA	3121
QY	378	CAGGCTCCAGCTGGTGACAGACCCGGCTTAGCCAGCAGCAGCAAGAGACACACATATCTC	437
DB	3122	CAGGCTCCAGCTGGTGACAGACCCGGCTTAGCCAGCAGCAGCAAGAGACACACATATCTC	3181
QY	438	CTGTGTCTGAGGCATGTGGCTTCGGAAGGATGCGGGCTTTACACTGCTGGGCCAAAA	497
DB	3182	CTGTGTCTGAGGCATGTGGCTTCGGAAGGATGCGGGCTTTACACTGCTGGGCCAAAA	3241
QY	498	CACGTGTGGCAGGTGCTCTGCAAGCAGAGGTGCTGGTGTCTGGGGGGGACAAATGAGCC	557
DB	3242	CACGTGTGGCAGGTGCTCTGCAAGCAGAGGTGCTGGTGTCTGGGGGGGACAAATGAGCC	3301
QY	558	GGACTCAGAGAAAGAACCCACCGAGAGAGCTGCACTCTTCTATAGAGTCAAGAGGA	617
DB	3302	GGACTCAGAGAAAGAACCCACCGAGAGAGCTGCACTCTTCTATAGAGTCAAGAGGA	3361
QY	618	GATTGGAAGGGGGTGTGGTTCGTAAGAGGTGACAGCAACAAAGAAACAAAGATCTT	677
DB	3362	GATTGGAAGGGGGTGTGGTTCGTAAGAGGTGACAGCAACAAAGAAACAAAGATCTT	3421
QY	678	GTGCGCTGCCAGTTATCCCTTACCGAGCAGAACTGGGGCCACAGGATACAGGAGCG	737
DB	3422	GTGCGCTGCCAGTTATCCCTTACCGAGCAGAACTGGGGCCACAGGATACAGGAGCG	3481
QY	738	AGACATCTGGCGCGCTGAGCCACCCGCTGTGTCAGGGGGCTGTGGACCAAGTTGAGAC	797
DB	3482	AGACATCTGGCGCGCTGAGCCACCCGCTGTGTCAGGGGGCTGTGGACCAAGTTGAGAC	3541
QY	798	CCGCAAGACCTCATCTCTATCTGTGAGCTGTGCTCATCCGAGGAGCTGTGGACCGCT	857
DB	3542	CCGCAAGACCTCATCTCTATCTGTGAGCTGTGCTCATCCGAGGAGCTGTGGACCGCT	3601
QY	858	GTACAGGAAGGGCGTGTGACGAGGCGCAGAGTCAAGGTCTACATCCAGCAGCTGGTGA	917
DB	3602	GTACAGGAAGGGCGTGTGACGAGGCGCAGAGTCAAGGTCTACATCCAGCAGCTGGTGA	3661
QY	918	GGGGCTGCATCTGACAGCCATGGCTTCTCCACCTGGACATAAAGCCCTCTAACAT	977
DB	3662	GGGGCTGCATCTGACAGCCATGGCTTCTCCACCTGGACATAAAGCCCTCTAACAT	3721
QY	978	CCTGATGGTGCATCTGCGCGGGAAGACATTAATAATCTGCGACTTTGGCTTGGCCAGAA	1037
DB	3722	CCTGATGGTGCATCTGCGCGGGAAGACATTAATAATCTGCGACTTTGGCTTGGCCAGAA	3781
QY	1038	CATCACCACAGCAGAGCTGAGTTACAGCAGTACGCTCCCTGAGTTGCTTCCCCCGA	1097
DB	3782	CATCACCACAGCAGAGCTGAGTTACAGCAGTACGCTCCCTGAGTTGCTTCCCCCGA	3841
QY	1098	GATCATCCAGCAAGACCTGTGAGCAAGCCTCCGACATTTGGGGCCATGGGTGTCTATCTC	1157
DB	3842	GATCATCCAGCAAGACCTGTGAGCAAGCCTCCGACATTTGGGGCCATGGGTGTCTATCTC	3901
QY	1158	CTACCTCAGCCTGACCTGCTCATCCCCCATTTTGGCGGCGAGGTGACCGTGCACCCCTCT	1217

DB	3902	CTACCTCAGCCTGACCTGCTCATCCCCCATTTGCGGGGAGAGTGACCGTGCACCCCTCT	3961
QY	1218	GAACTCTCTGGAGGGGCGCTGTGATGAGCAGAGCCCATATGCTGCCACCTCAGCGAAGA	1277
DB	3962	GAACTCTCTGGAGGGGCGCGTGTGATGAGCAGAGCCCATATGCTGCCACCTCAGCGAAGA	4021
QY	1278	CGCCAAAGACTTCAATCAAGGCTACGCTGACAGAGCCCTCAGGCCCGGCTAGTGGCG	1337
DB	4022	CGCCAAAGACTTCAATCAAGGCTACGCTGACAGAGAGCCCTCAGGCCCGGCTAGTGGCG	4081
QY	1338	CCAGTGTCTCTCCACCCCTGTTCTTCTGAAATCCATGCTGCGAGGAGGCGCCACTTCAT	1397
DB	4082	CCAGTGTCTCTCCACCCCTGTTCTTCTGAAATCCATGCTGCGAGGAGGCGCCACTTCAT	4141
QY	1398	CAACCCAAAGCAGCTCAAGTTCTTCTGCCCCGAAAGTCTGTCGAGGAGGCTTCCCTGATGAG	1457
DB	4142	CAACCCAAAGCAGCTCAAGTTCTTCTGCCCCGAAAGTCTGTCGAGGAGGCTTCCCTGATGAG	4201
QY	1458	CTACAAGTCCATCTCTGCTGATGCTCCATCTCTGCTGCGGGGCGCCACCCGACAG	1517
DB	4202	CTACAAGTCCATCTCTGCTGATGCTCCATCTCTGCTGCGGGGCGCCACCCGACAG	4261
QY	1518	CGCTCTCTCTGCGGTAGCCCGGACCTCTGAGGAGCACTGCTGCTGCTTCTTCTGCTTCTC	1577
DB	4262	CGCTCTCTCTGCGGTAGCCCGGACCTCTGAGGAGCACTGCTGCTGCTTCTTCTGCTTCTC	4321
QY	1578	CTCTCTCTCTGACAAACGAGCTCGCCCATTTTGGCGGGCTAAAGTCACTGCGCACCCCTCCC	1637
DB	4322	CTCTCTCTCTGACAAACGAGCTCGCCCATTTTGGCGGGCTAAAGTCACTGCGCACCCCTCCC	4381
QY	1638	GGTGACACACTCACCACCTGCTGCAACCCCGGGCTTCTGCGGGCTTCTGCGGCGCTGCG	1697
DB	4382	GGTGACACACTCACCACCTGCTGCAACCCCGGGCTTCTGCGGGCTTCTGCGGCGCTGCG	4441
QY	1698	TGAGGAAGCCGAGGCCAGTGAGCGCTCCACGAGGCCCCAGCTCCGCTGCATCTCCCGA	1757
DB	4442	TGAGGAAGCCGAGGCCAGTGAGCGCTCCACGAGGCCCCAGCTCCGCTGCATCTCCCGA	4501
QY	1758	GGTGACACACTCACCACCTGCTGCAACCCCGGGCTTCTGCGGGCTTCTGCGGCGCTGCG	1817
DB	4502	GGTGACACACTCACCACCTGCTGCAACCCCGGGCTTCTGCGGGCTTCTGCGGCGCTGCG	4561
QY	1818	GTCTTACCAACGAGCGGTGAGAGCCCTGAGACACGGGGCCCTTGGCCCGGGGAGAGCGG	1877
DB	4562	GTCTTACCAACGAGCGGTGAGAGCCCTTGGACACGGGGCCCTTGGCCCGGGGAGAGCGG	4621
QY	1878	GCACCGCGCGCGCGCGGCTGCTGCAAGGGCGGCTACATTTGCGGGGCGGCTGCCAGG	1937
DB	4622	GCACCGCGCGCGCGCGGCTGCTGCAAGGGCGGCTACATTTGCGGGGCGGCTGCCAGG	4681
QY	1938	CCTGCGCGAGCCACTGATGAGCAGCCGCTGCTGAGAGGAGGAGCCGCCAGGAGGAGCA	1997
DB	4682	CCTGCGCGAGCCACTGATGAGCAGCCGCTGCTGAGAGGAGGAGGAGCCGCCAGGAGGAGCA	4741
QY	1998	GGCGACCTCTCTGCGCAAGCCCTCATTTGAGACTGCTGCTGCGGCTGCTGCTCTGG	2057
DB	4742	GGCGACCTCTCTGCGCAAGCCCTCATTTGAGACTGCTGCTGCGGCTGCTGCTCTGG	4801
QY	2058	CACCCACTTTGGCCCTTGGCCACAGCACTCTCTGGAACATGACTCTCCGAGCAACCCCGG	2117
DB	4802	CACCCACTTTGGCCCTTGGCCACAGCACTCTCTGGAACATGACTCTCCGAGCAACCCCGG	4861
QY	2118	CCCTCTCTCGAGGCGCTGGGTGAGGACAGGACTGCTTACGCCCCCTCCCGGGGGGGC	2177
DB	4862	CCCTCTCTCGAGGCGCTGGGTGAGGACAGGACTGCTTACGCCCCCTCCCGGGGGGGC	4921
QY	2178	CCCTATCAGGGACATGGGGCACCTCAGGGCTTCAAGAGCTTCCATCCATGCTGAGGCA	2237
DB	4922	CCCTATCAGGGACATGGGGCACCTCAGGGCTTCAAGAGCTTCCATCCATGCTGAGGCA	4981
QY	2238	CCGAGGCACTGCTCAGCAGAGAGGCGCATCCCGGAGAGCCCTTGGGGGAGCGCCCGC	2297

QY	3378	ACGACGCTTTCCACTTCCCTGGGAGGCACTGCCGTGGATGAGCCTGCAGACTGGG	3437
Db	6122	ACGACGCTTTCCACTTCCCTGGGAGGACCTGCCGCTGATGAGCCTGCAGACTGGG	6181
QY	3438	GCTGCGTGAAGAGTGAAGGCTCCGTGGAGCACATCTCCCGATCCTGAAGGGCAGGCC	3497
Db	6182	GCTGCGTGAAGAGTGAAGGCTCCGTGGAGCACATCTCCCGATCCTGAAGGGCAGGCC	6241
QY	3498	GGAAAGCTTGGAGAGGAGGGGCCCCCGAGGAAGAGCCAGGCTTGCTTCTTCGCGCT	3557
Db	6242	GGAAAGCTTGGAGAGGAGGGGCCCCCGAGGAAGAGCCAGGCTTGCTTCTTCGCGCT	6301
QY	3558	CTCAGGCTGAAGAGCTGGAGCCGAGCGCGCAATTCCTAAGGAGCTCTCAGATCAGAC	3617
Db	6302	CTCAGGCTGAAGAGCTGGAGCCGAGCGCGCAATTCCTAAGGAGCTCTCAGATCAGAC	6361
QY	3618	TGTGHTCTGGCCAGTCACTGACACTGCGCTGCGAGTGTAGCCAGCCAGCTGCCCA	3677
Db	6362	TGTGHTCTGGCCAGTCACTGACACTGCGCTGCGAGTGTAGCCAGCCAGCTGCCCA	6421
QY	3678	GGCCACTGGAGCAAGACGGAGCCCCCTTGAGAGCAGCAGCGGTGCTCATCTCTGC	3737
Db	6422	GGCCACTGGAGCAAGACGGAGCCCCCTTGAGAGCAGCAGCGGTGCTCATCTCTGC	6481
QY	3738	CACCTCAAGAACTTCCAGCTTCTGACATCTCTGHTGHTGGCTGAGGACCTGGTGT	3797
Db	6482	CACCTCAAGAACTTCCAGCTTCTGACATCTCTGHTGHTGGCTGAGGACCTGGTGT	6541
QY	3798	GTACACTCGACGCTGAGCAATGCGCTGGGGACAGTGAACACACGGGCGTCTCCCGAA	3857
Db	6542	GTACACTCGACGCTGAGCAATGCGCTGGGGACAGTGAACACACGGGCGTCTCCCGAA	6601
QY	3858	GGCAGAGCGCCCTCATCTTCCCATGCCGATATCGGGAGGTGTACCGGATGGGT	3917
Db	6602	GGCAGAGCGCCCTCATCTTCCCATGCCGATATCGGGAGGTGTACCGGATGGGT	6661
QY	3918	GCTGCTGTCTGGAAGCCCGTGGAACTCTACGGCCCTGTGACCTACATTTGTCACTGCAGTGCAG	3977
Db	6662	GCTGCTGTCTGGAAGCCCGTGGAACTCTACGGCCCTGTGACCTACATTTGTCACTGCAGTGCAG	6721
QY	3978	CCTAGAAGCGCAGCTGACACACTGGCTCCGACACTCTTTGACTGCTGTACTGTAC	4037
Db	6722	CCTAGAAGCGCAGCTGACACACTGGCTCCGACACTCTTTGACTGCTGTACTGTAC	6781
QY	4038	CAGCAAGCTCTCCCGGGTGGCACTTACACTTCGCGACGGCATGTGTACGAAGCAGG	4097
Db	6782	CAGCAAGCTCTCCCGGGTGGCACTTACACTTCGCGACGGCATGTGTACGAAGCAGG	6841
QY	4098	AATGGTCTCCTACGAGCCCTCGGAGCAAGTCTCTTGGAGGGGCCAGCCACTGGC	4157
Db	6842	AATGGTCTCCTACGAGCCCTCGGAGCAAGTCTCTTGGAGGGGCCAGCCACTGGC	6901
QY	4158	CTCTGAGGAGGAGCCAGGGGCGGTAGCCCAAACCTTGCCTCCAGCAAAAGACCTTCGC	4217
Db	6902	CTCTGAGGAGGAGCCAGGGGCGGTAGCCCAAACCTTGCCTCCAGCAAAAGACCTTCGC	6961
QY	4218	ATTTCAGACACAGATCCAGAGGGGCGGTTCAGCGTGTGCGCAATGCTGGGAGAGGC	4277
Db	6962	ATTTCAGACACAGATCCAGAGGGGCGGTTCAGCGTGTGCGCAATGCTGGGAGAGGC	7021
QY	4278	CAGCGGGGCGGCGTGGCGCCAGAGATATCCCTTACACCCCAAAGACAGACGAGT	4337
Db	7022	CAGCGGGGCGGCGTGGCGCCAGAGATATCCCTTACACCCCAAAGACAGACGAGT	7081
QY	4338	GCTGCGCAATACGAGGCGCTCAAGGGCTTGGCCACCGCACCTTGGCCAGCTGCAGGC	4397
Db	7082	GCTGCGCAATACGAGGCGCTCAAGGGCTTGGCCACCGCACCTTGGCCAGCTGCAGGC	7141
QY	4398	AGCTTACTTCAGCCCGCGGCACTGGTGTCTATCTTTGAGCTGTGCTCTGGGCCGAGCT	4457
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RESULT 9
US-10-182-243-14
; Sequence 14, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCES: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

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RESULT 9
US-10-182-243-14
; Sequence 14, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCES: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

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Dd	3181	GAGCTGGGGCTG	CGTAGAGAGTGAAGGCTCCGTGGAGCA	CATCTCCGGATCCTGAAG	3240
Qy	3490	GGCAGGCGGAAGTCT	CGAAGAGGAGGGCCCCCGAGAGAGCAGAGCCTTGCTTC	3549	
Dd	3241	GGCAGGCGGAAGTCT	CGAAGAGGAGGGCCCCCGAGAGAGCAGAGCCTTGCTTC	3300	
Qy	3550	TTCCGGCTCTCAGTCT	CTGAAGAGCTGGGACCGAGCGCCGACATCTCTAAGGAGCTCTCA	3609	
Dd	3301	TTCCGGCTCTCAGTCT	CTGAAGAGCTGGGACCGAGCGCCGACATCTCTAAGGAGCTCTCA	3360	
Qy	3610	GATGAGACTGTGTCT	CGGCGCAGTCAGTGACACTGGCTGCGAGGTGTAGAGCCAGCCA	3669	
Dd	3361	GATGAGACTGTGTCT	CGGCGCAGTCAGTGACACTGGCTGCGAGGTGTAGAGCCAGCCA	3420	
Qy	3670	GCTGCCAGGCCA	CCTGGAGCAAGAGCGCGCCCTTGGAGAGCAGCGCGTGTCTC	3729	
Dd	3421	GCTGCCAGGCCA	CCTGGAGCAAGAGCGCGCCCTTGGAGAGCAGCGCGTGTCTC	3480	
Qy	3730	ATCTCTGCCACCCCTCA	AGAACTTCCAGCTTCTGACCATCTGGTGGTGGTGTAGAGAC	3789	
Dd	3481	ATCTCTGCCACCCCTCA	AGAACTTCCAGCTTCTGACCATCTGGTGGTGGTGTAGAGAC	3540	
Qy	3790	CTGGGTGTGTACA	CCTGCGAGGTGAGCAATGTGGCTTGGGACAGTGACCA	CGCGGCGTC	3849
Dd	3541	CTGGGTGTGTACA	CCTGCGAGGTGAGCAATGTGGCTTGGGACAGTGACCA	CGCGGCGTC	3600
Qy	3850	CTCCGGAAGGCAGAGCG	CCCTCATCTTGGCANTGCCGATATCGGAGAGGTGTACGG	3909	
Dd	3601	CTCCGGAAGGCAGAGCG	CCCTCATCTTGGCANTGCCGATATCGGAGAGGTGTACGG	3660	
Qy	3910	GATGGGTGTCTGTCT	GTGAAGCCCGTGGAAATCTTACGGCCCTGTGACCTACATTTGT	3969	
Dd	3661	GATGGGTGTCTGTCT	GTGAAGCCCGTGGAAATCTTACGGCCCTGTGACCTACATTTGT	3720	
Qy	3970	CAGTGCAGCTAGAAAG	CGGCGAGCTGGACCACTGGCTCCGACATCTTTGACTGTCTGC	4029	
Dd	3721	CAGTGCAGCTAGAAAG	CGGCGAGCTGGACCACTGGCTCCGACATCTTTGACTGTCTGC	3780	
Qy	4030	TACTGTACCGAGAGCTCT	CGCGGGTGGCACTACACCTTCGACGGCATGTGTACG	4089	
Dd	3781	TACTGTACCGAGAGCTCT	CGCGGGTGGCACTACACCTTCGACGGCATGTGTACG	3840	
Qy	4090	AAGCAGGAATGGGTCT	CTACAGCAGCCCTCGGAGCAAGTCTCTTGGAGGGCCCCAGC	4149	
Dd	3841	AAGCAGGAATGGGTCT	CTACAGCAGCCCTCGGAGCAAGTCTCTTGGAGGGCCCCAGC	3900	
Qy	4150	CACCTGGCTCTGAGAGG	AGAGCGAGGGCGGTGAGCCACCTTCGACCGCATGTGTACG	4209	
Dd	3901	CACCTGGCTCTGAGAGG	AGAGCGAGGGCGGTGAGCCACCTTCGACCGCATGTGTACG	3960	
Qy	4210	ACCTTCGCAATCCAGAC	CACAGATCCAGAGGGGCGCTTCAGCGTGGTGGCGCAATGTCTG	4269	
Dd	3961	ACCTTCGCAATCCAGAC	CACAGATCCAGAGGGGCGCTTCAGCGTGGTGGCGCAATGTCTG	4020	
Qy	4270	GAGAGGCGAGGGGCGG	CGCTGGCGCCCAAGATCATCTCCCTACACCCCAAGGACAG	4329	
Dd	4021	GAGAGGCGAGGGGCGG	CGCTGGCGCCCAAGATCATCTCCCTACACCCCAAGGACAG	4080	
Qy	4330	CACAGAGTGTCTGCG	GAATACAGGGCCCTCAAGGGCTTCGCGCACCTGGCCAG	4389	
Dd	4081	CACAGAGTGTCTGCG	GAATACAGGGCCCTCAAGGGCTTCGCGCACCTGGCCAG	4140	
Qy	4390	CTGCGACGAGCTACT	CTACGCCCCCGACCTGGTGTCTCATCTTGGAGCTGTGTCTGGG	4449	
Dd	4141	CTGCGACGAGCTACT	CTACGCCCCCGACCTGGTGTCTCATCTTGGAGCTGTGTCTGGG	4200	
Qy	4450	CCGAGCTGTCTCCCT	GTGCTGGCCGAGAGGGCTCTCTACTCAGATCTGAGGTGAAGAC	4509	
Dd	4201	CCGAGCTGTCTCCCT	GTGCTGGCCGAGAGGGCTCTCTACTCAGATCTGAGGTGAAGAC	4260	

RESULT 10

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US-10-077-130-3
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? Sequence 3, Application US/10077130
? Publication NO. US20020168742A1
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? GENERAL INFORMATION:
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? APPLICANT: Kapeller-Libermann, Rosana
?
? APPLICANT: Acton, Susan L.
?
? TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
?
? TITLE OF INVENTION: Members and Uses Therefor
?
? FILE REFERENCE: MPI2001-047E1RCP1(M)
?
? CURRENT APPLICATION NUMBER: US/10/077,130
?
? CURRENT FILING DATE: 2002-02-15
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? PRIOR APPLICATION NUMBER: 60/269201
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? PRIOR FILING DATE: 2001-02-15
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? NUMBER OF SEQ ID NOS: 9
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? SOFTWARE: FastSeq for Windows Version 4.0
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? SEQ ID NO 3
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? LENGTH: 7893
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? TYPE: DNA
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? ORGANISM: Homo sapiens
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? US-10-077-130-3

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Query Match 93.0%; Score 4841; DB 14; Length 7893;

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	Matches 4844; Conservative	0; Mismatches	5; Indels	0; Gaps	0;
Qy	258	CCGAGGGCCCCATTCATGCAGGTAACTCGAGGATGTGCAGGCACAGACGAGCGGAAC	317		
Dz	3045	CAGCAGGCCCATTCATGCAGGTAACTCGAGGATGTGCAGGCACAGACGAGCGGAAC	3104		
Qy	318	GSCCAATTTCAGGCTATCATTTAGGGCGCACCCACAGCCCTCGTGACTGGTACAAGA	377		
Dz	3105	GSCCAATTTCAGGCTATCATTTAGGGCGCACCCACAGCCCTCGTGACTGGTACAAGA	3164		
Qy	378	CAGCCTCAGCTGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGCACCACATACTC	437		
Dz	3165	CAGCCTCAGCTGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGCACCACATACTC	3224		
Qy	438	CCTGTGTCTGAGGCATGTGCCTCGAAGAGTCCGGCGTTACACTCGCTGGCCCABA	497		
Dz	3225	CCTGTGTCTGAGGCATGTGCCTCGAAGAGTCCGGCGTTACACTCGCTGGCCCABA	3284		
Qy	498	CACCTGGTGGCAGGTGCTCTGCAAGGCAGAGTGTGTGCTTGGGGGGGCAATGAGCC	557		
Dz	3285	CACCTGGTGGCAGGTGCTCTGCAAGGCAGAGTGTGTGCTTGGGGGGGCAATGAGCC	3344		
Qy	558	GGACTCAGAGAAGCAAAGCCACCGGAGGAAGTGCATCTTCTATGAGGTCAAGSAGGA	617		
Dz	3345	GGACTCAGAGAAGCAAAGCCACCGGAGGAAGTGCATCTTCTATGAGGTCAAGSAGGA	3404		
Qy	618	GATTGGGAAGGGCGTGTGGCTTGTAAGAAGTGCAGACAAAAGGAACAAGATCTT	677		
Dz	3405	GATTGGGAAGGGCGTGTGGCTTGTAAGAAGTGCAGACAAAAGGAACAAGATCTT	3464		
Qy	678	GTGCGCTGCCAAGTTTCATCCCTCAGGAGCAGACTCGGGCCAGGCAATACAGSGAGCG	737		
Dz	3465	GTGCGCTGCCAAGTTTCATCCCTCAGGAGCAGACTCGGGCCAGGCAATACAGSGAGCG	3524		
Qy	738	AGACATCTGCGCGGTGAGCAACCCGTGTGTCAGGGGGTGCTGAGCAGATTTGAGAC	797		
Dz	3525	AGACATCTGCGCGGTGAGCAACCCGTGTGTCAGGGGGTGCTGAGCAGATTTGAGAC	3584		
Qy	798	CGCGAAGACCTCATCTCTCATCTGTGAGGTGTCTCATCCGAGAGCTGTGTCAGCCGCT	857		
Dz	3585	CGCGAAGACCTCATCTCTCATCTGTGAGGTGTCTCATCCGAGAGCTGTGTCAGCCGCT	3644		
Qy	858	GTACAGGAAGGGCGTGTGACGAGGCGGAGGTCAAGGTCTACATCMAGCAGCTGTGTGGA	917		
Dz	3645	GTACAGGAAGGGCGTGTGACGAGGCGGAGGTCAAGGTCTACATCMAGCAGCTGTGTGGA	3704		
Qy	918	GGGGCTGCACCTAACCTGCACAGGCATGGCGTTTCCAACCTGGACATAAAGCCCTCTAACAT	977		
Dz	3705	GGGGCTGCACCTAACCTGCACAGGCATGGCGTTTCCAACCTGGACATAAAGCCCTCTAACAT	3764		
Qy	978	CCTGATGTGATCTCTCCCGGGAAGCAATTAANCTGCGACTTTGCTTTGGCCAGAA	1037		
Dz	3765	CCTGATGTGATCTCTCCCGGGAAGCAATTAANCTGCGACTTTGCTTTGGCCAGAA	3824		
Qy	1038	CATCACCCCGACAGAGCTGCAGTTTCAGCCAGATACGGCTCCCTCGATTCCTCCCGCA	1097		
Dz	3825	CATCACCCCGACAGAGCTGCAGTTTCAGCCAGATACGGCTCCCTCGATTCCTCCCGCA	3884		
Qy	1098	GATCATCCAGCAGAACCTGTGAGCGAAGCTCTCGACATTTGGGGCCATGGGTGTATCTC	1157		
Dz	3885	GATCATCCAGCAGAACCTGTGAGCGAAGCTCTCGACATTTGGGGCCATGGGTGTATCTC	3944		
Qy	1158	CTACCTCAGCCTGACCTGTCTATCCCAATTTGCCCGCGAGAGTGACCGTGCCACCTCT	1217		
Dz	3945	CTACCTCAGCCTGACCTGTCTATCCCAATTTGCCCGCGAGAGTGACCGTGCCACCTCT	4004		
Qy	1218	GNAAGTCTGAGGGGGCGGTGTCTATGAGAGCGACCCCATGGCTGCCNACCTCAGCNAGA	1277		
Dz	4005	GAAAGTCTGAGGGGGCGGTGTCTATGAGAGCGACCCCATGGCTGCCNACCTCAGCNAGA	4064		
Qy	1278	CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCTCAGGCGCGGGCTAGTGC	1337		

4065	CGCCAAAGACTTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCCCGGCTTAGTGGCGC	4124
1338	CCAGTGCCTCTCCCAACCCCTGGTTCCTGAAATCCATGCTCGGAGGAGGCCCACTTCAT	1397
4125	CCAGTGCCTCTCCCAACCCCTGGTTCCTGAAATCCATGCTCGGAGGAGGCCCACTTCAT	4184
1398	CAACACCAAGCAGCTCAAGTTCCTCTCGCCCGAAGTGCCTGGCAGCGTTCCTCATGATGAG	1457
4185	CAACACCAAGCAGCTCAAGTTCCTCTCGCCCGAAGTGCCTGGCAGCGTTCCTCATGATGAG	4244
1458	CTACAAGTCCATCTCTGGTGAAGCGCTCCATCCCTGAGTGTGTGCGGGGCCCAACCCGACAG	1517
4245	CTACAAGTCCATCTCTGGTGAAGCGCTCCATCCCTGAGTGTGTGCGGGGCCCAACCCGACAG	4304
1518	CCCTCCCTCGGCGTAGCCCGGCACCTCTGCAGGAGACACTGGTGGCTCTCTCCAGTTCCTC	1577
4305	CCCTCCCTCGGCGTAGCCCGGCACCTCTGCAGGAGACACTGGTGGCTCTCTCCAGTTCCTC	4364
1578	CTCTCTCTGTGACAACGAGACTCGCCCCCATTTTGCCCGGGCTAAGTCACTGCGCAACCTTCGCC	1637
4365	CTCTCTCTGTGACAACGAGACTCGCCCCCATTTTGCCCGGGCTAAGTCACTGCGCAACCTTCGCC	4424
1638	GGTGACACACTCACCACTGCTGCACACCCCGGGGCTTCCTGCGGCCCTCGGCCAGAGCTGCC	1697
4425	GGTGACACACTCACCACTGCTGCACACCCCGGGGCTTCCTGCGGCCCTCGGCCAGAGCTGCC	4484
1698	TGAGGAAGCCGAGGCGAGTGAGCGGTCCACCGAGGCCCCAGCTCCGCTGTGATCTCCCGA	1757
4485	TGAGGAAGCCGAGGCGAGTGAGCGGTCCACCGAGGCCCCAGCTCCGCTGTGATCTCCCGA	4544
1758	GGGTGCCGGGCCACCGCGCGCCCGGAGGCTCGGTGCCCGGGCACACGCTCATCCGCAAGCT	1817
4545	GGGTGCCGGGCCACCGCGCGCCCGGAGGCTCGGTGCCCGGGCACACGCTCATCCGCAAGCT	4604
1818	GTTCTACCAACGAGGCGGTGAGAGCCCTGTAGACAACGGGCGCTTGGGCCCGGGAGCAGGCG	1877
4605	GTTCTACCAACGAGGCGGTGAGAGCCCTGTAGACAACGGGCGCTTGGGCCCGGGAGCAGGCG	4664
1878	GCAACCCGGCCCCGGCGGCGCACTGCTGAAAGGGCGGCTACATTTGCGGGGGCGCTGCCAGG	1937
4665	GCAACCCGGCCCCGGCGGCGCACTGCTGAAAGGGCGGCTACATTTGCGGGGGCGCTGCCAGG	4724
1938	CTTGCGGAGCCACTGATGGAGCACCGGTGCTGAGGAGGAGGSCCGCCAGGGAGGAGCA	1997
4725	CTTGCGGAGCCACTGATGGAGCACCGGTGCTGAGGAGGAGGSCCGCCAGGGAGGAGCA	4784
1998	GGCCACCTCTCTGGCCAAAGCCCCCTCATTTGAGACTGCCCCCTCCGGCTGCCTCTCTGG	2057
4785	GGCCACCTCTCTGGCCAAAGCCCCCTCATTTGAGACTGCCCCCTCCGGCTGCCTCTCTGG	4844
2058	GACCCACTTTGGCCCCCTGGGCCACAGGCACTCCCTGGAACATGACTCTCCGAGCAACCCCCG	2117
4845	GACCCACTTTGGCCCCCTGGGCCACAGGCACTCCCTGGAACATGACTCTCCGAGCAACCCCCG	4904
2118	CCCTCTCTCGGAGGCGCTCGGCTGAGGACACAGCGACTGCTCTTCAGCCCCCTCCGGGGGGGC	2177
4905	CCCTCTCTCGGAGGCGCTCGGCTGAGGACACAGCGACTGCTCTTCAGCCCCCTCCGGGGGGGC	4964
2178	CCCTATCAGGACATGGGGCACCTTCAGGCTCCAGAGCTTCATCCACTGTGGGGCA	2237
4965	CCCTATCAGGACATGGGGCACCTTCAGGCTCCAGAGCTTCATCCACTGTGGGGCA	5024
2238	CCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGACAGCCCTTTGGGGGCGAGCCAGCCCC	2297
5025	CCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGACAGCCCTTTGGGGGCGAGCCAGCCCC	5084
2298	TTTTCTGGCAACCCCAAGAGGGTTCTGCCCCCAGAGAGGCGTGCAGCCCCCAACAGCAGT	2357
5085	TTTTCTGGCAACCCCAAGAGGGTTCTGCCCCCAGAGAGGCGTGCAGCCCCCAACAGCAGT	5144
2358	TGCCCCATGCCCTCTCTGGCTCTCTCCCTCCAGGATCTTTGCAAGAGGCCCTCTTAGTACC	2417
5145	TGCCCCATGCCCTCTCTGGCTCTCTCCCTCCAGGATCTTTGCAAGAGGCCCTCTTAGTACC	5204

QY	2418	CTCAAGCCCTTCTTTGGACAGCCCAAGGCACCCCTGCCCCTGCGCAAGCAAGCAAGCCGCC	2477
Db	5205	CTCAAGCCCTTCTTTGGACAGCCCAAGGCACCCCTGCCCCTGCGCAAGCAAGCAAGCCGCC	5264
QY	2478	ATTGACTCTAAGATGGGGCTTGAGACATCTCTTTCTGGAGGCCAAAACCGCGGCC	2537
Db	5265	ATTGACTCTAAGATGGGGCTTGAGACATCTCTTTCTGGAGGCCAAAACCGCGGCC	5324
QY	2538	CTGAGTTCCCAAGGCTCAGGCTCCAGGCGAGCTCTTCCAACTGAGTCCCTCAGGCT	2597
Db	5325	CTGAGTTCCCAAGGCTCAGGCTCCAGGCGAGCTCTTCCAACTGAGTCCCTCAGGCT	5384
QY	2598	GGGCTCTCCAGGTGGGCACAGAGCCTGGCCCCCTCTCTGATGCGGAGGCTGACCCCA	2657
Db	5385	GGGCTCTCTCCAGGTGGGCACAGAGCCTGGCCCCCTCTCTGATGCGGAGGCTGACCCCA	5444
QY	2658	GGAGGCTCAGAGTCTGTCCGACTCCACACCACTTGAGAGCGGCTCAGGAACAGGTGAC	2717
Db	5445	GGAGGCTCAGAGTCTGTCCGACTCCACACCACTTGAGAGCGGCTCAGGAACAGGTGAC	2776
QY	2718	CATGCGCAAGTTCTCCCTGGGTGGTGGCGGGCTACGAGCGTGGCTGGCTATGSCAC	2777
Db	5505	CATGCGCAAGTTCTCCCTGGGTGGTGGCGGGCTACGAGCGTGGCTGGCTATGSCAC	5564
QY	2778	CTTTCCCTTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT	2837
Db	5565	CTTTCCCTTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT	5624
QY	2838	AGCCTGGGCTGTGTCCCATGTGGAGAGAGAGCAGAGAGGCGCAGGGCTGAGTCCCA	2897
Db	5625	AGCCTGGGCTGTGTCCCATGTGGAGAGAGAGCAGAGAGGCGCAGGGCTGAGTCCCA	5684
QY	2898	GTGCGAGGACAGCAGGAGGCGCAGGGCTGAGAGCCCATCGCCCCAGGTCACTGCAAGGCC	2957
Db	5685	GTGCGAGGACAGCAGGAGGCGCAGGGCTGAGAGCCCATCGCCCCAGGTCACTGCAAGGCC	5744
QY	2958	TGTGCTCAGGCTCGCAGGGCTCCACAGGAGCTCTCCAGAGCCACCCCATGGAGGA	3017
Db	5745	TGTGCTCAGGCTCGCAGGGCTCCACAGGAGCTCTCCAGAGCCACCCCATGGAGGA	5804
QY	3018	CATCGGCGAGGCTCTCCCTGGTGAGATCCGGGACCTGTGAGGTGATCGGAGGCGGCCGA	3077
Db	5805	CATCGGCGAGGCTCTCCCTGGTGAGATCCGGGACCTGTGAGGTGATCGGAGGCGGCCGA	5864
QY	3078	CACAATATCCTTGAGACATTTCCGAGGTGACCCCGCTACCTCACTCTCAGACCTGTA	3137
Db	5865	CACAATATCCTTGAGACATTTCCGAGGTGACCCCGCTACCTCACTCTCAGACCTGTA	5924
QY	3138	CGATATCAAGTACTCTCCATTCGAGTTTATGATTTTCAGGAAAGTCCCAAGTCCGCTCA	3197
Db	5925	CGATATCAAGTACTCTCCATTCGAGTTTATGATTTTCAGGAAAGTCCCAAGTCCGCTCA	5984
QY	3198	GCCAGACCGCCCTCCCCCATGGTGGAGAGAGCTGGCGGATTCGCGAGCCCAAGTGTG	3257
Db	5985	GCCAGACCGCCCTCCCCCATGGTGGAGAGAGCTGGCGGATTCGCGAGCCCAAGTGTG	6044
QY	3258	GCCCTGGCCAGGTGAATGGGCCCCACGCGAGCTGGAGATCAAGAGGAGTCAAGAGGA	3317
Db	6045	GCCCTGGCCAGGTGAATGGGCCCCACGCGAGCTGGAGATCAAGAGGAGTCAAGAGGA	6104
QY	3318	TGTGACACGCTGTGTGCGAGAGGCTGCGGTGGGAGGAGCGCAAGTGGTCTTCGCGCTC	3377
Db	6105	TGTGACACGCTGTGTGCGAGAGGCTGCGGTGGGAGGAGCGCAAGTGGTCTTCGCGCTC	6164
QY	3378	AGCGAGCCTCTCCACTTCCCTGGGAGGACCTGCGCTGGATGAGCTGAGAGGCTGG	3437
Db	6165	AGCGAGCCTCTCTCCACTTCCCTGGGAGGACCTGCGCTGGATGAGCTGAGAGGCTGG	6224
QY	3438	GCTCGTGGAGAGTGAAGGCTCCCTGGGACACATCTCCCGGATCTCTGAAGGGCAGGCC	3497
Db	6225	GCTCGTGGAGAGTGAAGGCTCCCTGGGAGGACATCTCCCGGATCTCTGAAGGGCAGGCC	6284

QY	3498	GGAAAGCTCTGGAGAAAGAGGGGCCCCCCACAGAAAGACGAGCCCTTGTCTCTCTCCGGCT	3557
DB	6285	GGAAAGCTCTGGAGAAAGAGGGGCCCCCCACAGAAAGACGAGCCCTTGTCTCTCTCCGGCT	6344
QY	3558	CTCAGGTCTGAAGAGCTGGGACCGGAGCGCGACATTTCTAAAGGAGCTCTCAGATGAGAC	3617
DB	6345	CTCAGGTCTGAAGAGCTGGACCGGAGCGCGACATTTCTAAAGGAGCTCTCAGATGAGAC	6404
QY	3618	TGTGGTCTTGGGCCAGTCACTGCTGCTGCCAGTGTTCAGCCACGACGCTGCCCA	3677
DB	6405	TGTGGTCTTGGGCCAGTCACTGCTGCTGCCAGTGTTCAGCCACGACGCTGCCCA	6464
QY	3678	GGCCACTCTGGAGCAAGACCGGAGCGCCCTCTGGAGAGCAGACCGTGTCTCTCATCTCTGC	3737
DB	6465	GGCCACTCTGGAGCAAGACCGGAGCGCCCTCTGGAGAGCAGACCGTGTCTCTCATCTCTGC	6524
QY	3738	CACGCTCAAGAACTTCCAGTCTTGACCAATCCTGGTGGTGGCTGAGGACCTGGGATGT	3797
DB	6525	CACGCTCAAGAACTTCCAGTCTTGACCAATCCTGGTGGTGGCTGAGGACCTGGGATGT	6584
QY	3798	GTACACTCTCAGCGTAGCAATGCGCTGGGACAGTAGACCAACGCGCGCTCTCCCGAA	3857
DB	6585	GTACACTCTCAGCGTAGCAATGCGCTGGGACAGTAGACCAACGCGCGCTCTCCCGAA	6644
QY	3858	GGCAGAGCGCCCTCATCTTCCACCATGCCCGGATATCGGGAGGTGTACCGGATGGGT	3917
DB	6645	GGCAGAGCGCCCTCATCTTCCACCATGCCCGGATATCGGGAGGTGTACCGGATGGGT	6704
QY	3918	GCTGCTGGTCTGGAAGCCCGTGGAAATCTTACGGCCCTGTGACCTACATTTGTGCACTCAG	3977
DB	6705	GCTGCTGGTCTGGAAGCCCGTGGAAATCTTACGGCCCTGTGACCTACATTTGTGCACTCAG	6764
QY	3978	CCTAGAAGCGGACGTGAGCACACTGGCTTCGACATCTTTGACTGTGCTACCTTGAC	4037
DB	6765	CCTAGAAGCGGACGTGAGCACACTGGCTTCGACATCTTTGACTGTGCTACCTTGAC	6824
QY	4038	CAGCAAGCTCTCCGGGTGGCACTTACCTTCGCACGGCATGTGTCAAGCAAGGCAAG	4097
DB	6825	CAGCAAGCTCTCCGGGTGGCACTTACCTTCGCACGGCATGTGTCAAGCAAGGCAAG	6884
QY	4098	AATGGGTCCCTACAGCAGCCCTCGGACCAAGTCTCTCTGGAGGGGCCAGCACCTTGC	4157
DB	6885	AATGGGTCCCTACAGCAGCCCTCGGACCAAGTCTCTCTGGAGGGGCCAGCACCTTGC	6944
QY	4158	CTCTGAGGAGAGACGAGGGCGGTTCAGCCCAACCCCTGCCCCAGCAAGACCTTTCGC	4217
DB	6945	CTCTGAGGAGAGACGAGGGCGGTTCAGCCCAACCCCTGCCCCAGCAAGACCTTTCGC	7004
QY	4218	ATTCCAGACACAGATCCAGAGGGCGGTTCAGCGTGGTGGCGCAATGCTGGAGAGAGC	4277
DB	7005	ATTCCAGACACAGATCCAGAGGGCGGTTCAGCGTGGTGGCGCAATGCTGGAGAGAGC	7064
QY	4278	CACGGGCGGCGCTGGCGCCAGATCATCCCTTACACCCCAAGAGCAAGACAGCAGT	4337
DB	7065	CACGGGCGGCGCTGGCGCCAGATCATCCCTTACACCCCAAGAGCAAGACAGCAGT	7124
QY	4338	GCTGGCGAATACGAGGCCCTCAGAGGCCCTGCGCCACCCGACCTTGGCCACAGCTGCAACGC	4397
DB	7125	GCTGGCGAATACGAGGCCCTCAGAGGCCCTGCGCCACCCGACCTTGGCCACAGCTGCAACGC	7184
QY	4398	AGCCTACTCAGCCCCGGGCACTGGTGGCTCATCTTGGAGCTGTGCTCTGGGCCCGAGCT	4457
DB	7185	AGCCTACTCAGCCCCGGGCACTGGTGGCTCATCTTGGAGCTGTGCTCTGGGCCCGAGCT	7244
QY	4458	GCTCCCTCGCTGGCCGAGAGGCCCTCTTACTCAGAAFTCTGAGTGAAGGACTACCTGTG	4517
DB	7245	GCTCCCTCGCTGGCCGAGAGGCCCTCTTACTCAGAAFTCTGAGTGAAGGACTACCTGTG	7304
QY	4518	GCAGATGTTAGTGCCACCCAGTACTGCAACACGACACATCTCTGCACTCTGGACCTGAG	4577
DB	7305	GCAGATGTTAGTGCCACCCAGTACTGCAACACGACACATCTCTGCACTCTGGACCTGAG	7364
QY	4578	GTCCGAGAACATGATCATCACCGAATACAACTGCTCAAGTCTGTGACCTGGGCAATGC	4637

Db	7365	GTCCGAGAA	CATGATCATCACCGAATACAACTGCTCAAGGTCTGGACCTGGGCATGC	7424
QY	4638	ACAGAGCCTCAGCCAGAGAGAGGTGTGCGCTTCAGACAAGTTCAGGACTACCTAGAGAC	4697	
Db	7425	ACAGAGCCTCAGCCAGGAGAGGTGTGCGCTTCAGACAAGTTCAGGACTACCTAGAGAC	7484	
QY	4698	CATGGCTCCAGAGACTCTGTGAGGGGCGAGGGGGCTGTTCCACAGACACACATCTGGGCCAT	4757	
Db	7485	CATGGCTCCAGAGACTCTGTGAGGGGCGAGGGGCTGTTCCACAGACACACATCTGGGCCAT	7544	
QY	4758	CGGTGTGACAGCCCTTCATCATGCTGAGCGCGAGATACCCGGTGAAGAGAGGGTGCACG	4817	
Db	7545	CGGTGTGACAGCCCTTCATCATGCTGAGCGCGAGATACCCGGTGAAGAGAGGGTGCACG	7604	
QY	4818	CGACCTCAGAGAGGACTCGCAAGGGGCTGTGCGGTGAGCCGCTGTCTACGCGGGGT	4877	
Db	7605	CGACCTCAGAGAGGACTCGCAAGGGGCTGTGCGGTGAGCCGCTGTCTACGCGGGGT	7664	
QY	4878	GTCCGGGGGGCGCGTGGCTTCTCTCGGACAGACTCTGTGCGCCACGCTGGGGCGGCC	4937	
Db	7665	GTCCGGGGGGCGCGTGGCTTCTCTGGACAGACTCTGTGCGCCACGCTTGGGGCGGCC	7724	
QY	4938	GTGCGCTCCAGCTGCTCAGTGGCCGTGGCTTAACAGAGAGGGCCCGCTGTTCGCG	4997	
Db	7725	GTGCGCTCCAGCTGCTCAGTGGCCGTGGCTTAACAGAGAGGGCCCGCTGTTCGCG	7784	
QY	4998	GCCCGCCCGTGCACCTTCCTTACCGCGGGCTGGCGTCTTGTGCGCAATCGCGAGAA	5057	
Db	7785	GCCCGCCCGTGCACCTTCCTTACCGCGGGCTGGCGTCTTGTGCGCAATCGCGAGAA	7844	
QY	5058	GAGACGCGCGCTGCTGTATCAAGAGGACAACCTGGCCAGGTGGCTGA	5106	
Db	7845	GAGACGCGCGCTGCTGTATCAAGAGGACAACCTGGCCAGGTGGCTGA	7893	

RESULT 11

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US-10-077-130-6
; Sequence 6, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047p1RCp1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-130-6

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QY	258	CCACAGGGCCCCATCCATCAGAGTAAACCATCGAGGTGTGCAGGCACACACAGGGCGAAC	317		
Db	19059	CGCACGGCCCCCATCCATCAGAGTAAACCATCGAGGTGTGCAGGCACACAGGGCGAAC	19118		
QY	318	GGCCCAATTTCAGGGCTTATCATTTAGGGGGGACCCACAGCCCTTCGGTACCTGGTACAAGGA	377		
Db	19119	GGCCCAATTTCAGGGCTTATCATTTAGGGGGACCCACAGCCCTTCGGTACCTGGTACAAGGA	19178		
QY	378	CAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAGGCCACACATATCTC	437		
Db	19179	CAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAGGCCACACATATCTC	19238		

QY 1518 CCCCTCCCTCGGCTAGCCCGGCACTCTGCAAGGCACTGTGGCTCTCCAGTTCTCTC 1577
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QY 1578 CTCCTCTCTGACAAAGAGCTCGCCCAATTTGCCCGGCTAAGTCACTGCGCACTCTCC 1637
Db 20379 CTCCTCTCTGACAAAGAGCTCGCCCAATTTGCCCGGCTAAGTCACTGCGCACTCTCC 20438
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Db 20439 GGTGACACACTCACTGCTGCAACCCCGGGGCTTTCTGCGGCTCTGCGCAGCTGCC 20498
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QY 1818 GTTCTACCAACAGCGGGGTGAGAGCCCTGAGCAACCGGGGCTTGGCCCGGGAGCAGGCG 1877
Db 20619 GTTCTACCAACAGCGGGGTGAGAGCCCTGAGCAACCGGGGCTTGGCCCGGGAGCAGGCG 20678
QY 1878 GCACCCGCGCGCGGCGGCACTGCTGAGGGCGCTACATTTGGGGGGCTGCTCAGG 1937
Db 20679 GCACCCGCGCGCGGCGGCACTGCTGAGGGCGGCTACATTTGGGGGGCTGCTCAGG 20738
QY 1938 CCTCGCGAGCACTGATGAGCAACCGCTGCTGAGGAGGAGGCGCGCAGGAGGAGCA 1997
Db 20739 CCTCGCGAGCACTGATGAGCAACCGCTGCTGAGGAGGAGGCGCGCAGGAGGAGCA 20798
QY 1998 GGCACACCTCTGSCAAAGCCCTCATTTCCGAGCTGCTCCGCTGCTGCTG 2057
Db 20799 GGCACACCTCTGSCAAAGCCCTCATTTCCGAGCTGCTCCGCTGCTGCTG 20858
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Db 21159 TGCCCCATGCTCTCTGCTCTCTCCCTCAGGATCTTGCAGAGGCGCCCTTAGTACC 21218
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Db 21219 CTCAGGCGCTCTTGTGGGACAGCCCGCAGGCAACCCCTGCTGCGCAAGCAAGCCGCC 21278
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Db 21459 GAGGCTGAGATCTGTCCGACTCCACACCACTTGCAGGCGCTCAGGAAAGGTGAC 21518
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Db 22179 AGCAGCTCTTTCATCTTCCCTGAGGAGGCTGCGCGCTGAGTGAAGCTGCGAGGCTGG 22238
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QY 3618 TGTGCTCTGCGGCGCAGTCACTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 3677
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Db 22479 GGCACCTGGAGCAAGACGAGAGCCCTCTGGAGAGCAGCCGCTGCTCATCTCTGC 22538
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Db 22539 CACCTCAAGAACTTCAGACTTCTGACCATCTGGTGGTGGCTGAGGACTGGGTGT 22598
Qy 3798 GTACACTGACAGGTGAGCAATGCGCTGGGGAAGTGAACAACAAGGCGTCTCCGAA 3857
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Qy 3858 GGCAGAGCGCCCTCATCTTCGCGATGCGCCGAGATATCGGGAGGTGTACCGCGATGGGT 3917
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Qy 3918 GCTGCTGCTGAGAGCGCCCTGGAATCTTACGCGCTGTGAACCTATTTGTCAGTGCAG 3977
Db 22719 GCTGCTGCTGAGAGCGCCCTGGAATCTTACGCGCTGTGAACCTATTTGTCAGTGCAG 22778
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Qy 4278 CAGGGCGGGCGCTGCGCCCAAGATCATCTCCCTACCAACCCCAAGAGCAAGAGCAGT 4337
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Qy 4338 GCTGCGGGAATAGAGGCGCTCAAGGCGCTGGCCACCGCCACTGGCCAGCTCAGCG 4397
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Db 23499 CATGGCTCCAGAGCTCTGAGGGGCGAGGGGCTGTTCACAGACAGACATCTGGGCCAT 23558
Qy 4758 CGGTGTGACAGCTTTCATCATGCTGAGCGCCGAGTACCGGCTGAGCAGCGAGGTGCACG 4817
Db 23559 CGGTGTGACAGCTTTCATCATGCTGAGCGCCGAGTACCGGCTGAGCAGCGAGGTGCACG 23618

Qy 4818 CGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTTCGGCTGAGCCGCTGCTACCGGGCT 4877
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Qy 4878 GTCCGGGGCGCGCTGGCTTCTCTGCGAGCACTCTGTGCGGCCAGCCCTGSGGCGCGGC 4937
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Qy 4938 CTCGGGCTGCAGCTGCTGCTGAGTGGCCGCTGCTAAACAGAGAGGGCGCGGCTGTTCGG 4997
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Qy 4998 GCGCGCGCGCTGACCTTCCCTACCGCGGCTGCGGCTTTCGTGCGCAATTCGAGAA 5057
Db 23799 GCGCGCGCGCTGACCTTCCCTACCGCGGCTGCGGCTTTCGTGCGCAATTCGAGAA 23858
Qy 5058 GAGACGCGGCTGCTGTACAAGAGGCAACCTTGGCCCGAGGTGCGCTCA 5106
Db 23859 GAGACGCGGCTGCTGTACAAGAGGCAACCTTGGCCCGAGGTGCGCTCA 23907

RESULT 12

US-10-307-019-2
; Sequence 2, Application US/10307019
; Publication No. US2003010853A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stancon, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DW1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4175
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4053)
US-10-307-019-2

Query Match 79.6%; Score 4146.6; DB 15; Length 4175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4149; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1055 TGCAGTTACGCCAGTACCGCTCCCTGAGTTGCTTCCCGAGATCATCCAGAGAAC 1114
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Qy 1115 CTGTGAGCGAAGCTCCGACATTTGGGCGCATGGGTGTCTCTCTTACCTCAGCCTGACCT 1174
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Qy 1175 GCTCATCCCCATTTCCGCGCGAGAGTACCGTCCCACTCTCTGAACTCTCTGAGGGGC 1234
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Qy 1235 GCGTGTCTGAGAGCAGCCCATGGTGGCCCACTCTCAGCGAAGAGCCCAAGACTTCATCA 1294
Db 185 GCGTGTCTGAGAGCAGCCCATGGTGGCCCACTCTCAGCGAAGAGCCCAAGACTTCATCA 244
Qy 1295 AGCTACGCTGAGAGAGCCCTCAGGCGCGGCTGTGCGGCGGCTGCTCTCCAC 1354
Db 245 AGCTACGCTGAGAGAGCCCTCAGGCGCGGCTGTGCGGCGGCTGCTCTCCAC 304

1355	QY	CCTGGTTCCTGAATTCATGCCTCGCGAGGAGGCCACACTTCATCAACCAAGCAGCTCA	1414
305	DB	CCTGGTTCCTGAATTCATGCCTCGCGAGGAGGCCACACTTCATCAACCAAGCAGCTCA	364
1415	QY	AGTTCTCTCTGGCCCGGAAGTCGCTGGCAGCGTTCCCTGATGAGCTTACAAGTCCATCTCGG	1474
365	DB	AGTTCTCTCTGGCCCGGAAGTCGCTGGCAGCGTTCCCTGATGAGCTTACAAGTCCATCTCGG	424
1475	QY	TGATCGCGTCCATCCCTTGAGCTGCTGCGGGGCCACCCGACAGACCCCTCCCTCGGCGTAG	1534
425	DB	TGATCGCGTCCATCCCTTGAGCTGCTGCGGGGCCACCCGACAGACCCCTCCCTCGGCGTAG	484
1535	QY	CCGGCACCCTCTGCAGGGACACTGGTGGGCTTCCTCCAGTTCTCTCTCTCTCTCTGACAAAG	1594
485	DB	CCGGCACCCTCTGCAGGGACACTGGTGGGCTTCCTCCAGTTCTCTCTCTCTCTGACAAAG	544
1595	QY	AGCTCGCCCATTTGCCCGGCTAAAGTCACTGCGACCCCTCCCGGTGACACACTCAACC	1654
545	DB	AGCTCGCCCATTTGCCCGGCTAAAGTCACTGCGACCCCTCCCGGTGACACACTCAACC	604
1655	QY	TGCTGCACCCCGGGGCTTCCTCGGCCCTCGGCCAGGCTGCTGAGGAAGCGAGGCCA	1714
605	DB	TGCTGCACCCCGGGGCTTCCTCGGCCCTCGGCCAGGCTGCTGAGGAAGCGAGGCCA	664
1715	QY	GTGAGCGCTCCACGAGGCCACAGCTCCGCGTGCATCTCCGAGGGTGC CGGGCACCGG	1774
665	DB	GTGAGCGCTCCACGAGGCCACAGCTCCGCGTGCATCTCCGAGGGTGC CGGGCACCGG	724
1775	QY	CCGCCACAGGGTCGTCGCCCGGCACAGGCTCATCCGACGCTGTCTTACCAACAGGCGG	1834
725	DB	CCGCCACAGGGTCGTCGCCCGGCACAGGCTCATCCGACGCTGTCTTACCAACAGGCGG	784
1835	QY	GTGAGAGCCCTTGACACGCGGGCCCTGGCCCCGGGGAGCAGCGGCACCCGGCCCGGGCG	1894
785	DB	GTGAGAGCCCTTGACACGCGGGCCCTGGCCCCGGGGAGCAGCGGCACCCGGCCCGGGCG	844
1895	QY	GGCACTGTCTGAAGGGCGGCTACATTCGGGGGGCGCTGCAGGCGTGC CGGAGCACTGA	1954
845	DB	GGCACTGTCTGAAGGGCGGCTACATTCGGGGGGCGCTGCAGGCGTGC CGGAGCACTGA	904
1955	QY	TGGAGCACCGCGTCTGGAGAGAGGCGCGCCAGAGGAGAGCAGGCCACCTCTGSCCA	2014
905	DB	TGGAGCACCGCGTCTGGAGAGAGGCGCGCCAGAGGAGAGCAGGCCACCTCTGSCCA	964
2015	QY	AAGCCCTCATTTGAGACTGCGCTTCGGCTGCTCTTGBCACCGACTTGGCCCGCTG	2074
965	DB	AAGCCCTCATTTGAGACTGCGCTTCGGCTGCTCTTGBCACCGACTTGGCCCGCTG	1024
2075	QY	GCCACAGCACTCCCTGGAACTGACTCTCCGAGACACCCCGCGCCCTCTCTCGAGGCGCT	2134
1025	DB	GCCACAGCACTCCCTGGAACTGACTCTCTCGAGACACCCCGCGCCCTCTCTCGAGGCGCT	1084
2135	QY	CGGTGAGGCACAGCACTGCCCTTACGCCCCCTCGGGGGGGCCCCCTATCAGGGACATGG	2194
1085	DB	CGGTGAGGCACAGCACTGCCCTTACGCCCCCTCGGGGGGGCCCCCTATCAGGGACATGG	1144
2195	QY	GGCACCCCTCAGGGCTCCACGACGCTTCACACTGGTGGGCACCGCAGGACACTGCTCAGC	2254
1145	DB	GGCACCCCTCAGGGCTCCACGACGCTTCACACTGGTGGGCACCGCAGGACACTGCTCAGC	1204
2255	QY	CAGAGAGCCATCCCGGACAGCCCTTGGGGGAGCGCACGCCCTTTCTGCCCCCAAGC	2314
1205	DB	CAGAGAGCCATCCCGGACAGCCCTTGGGGGAGCGCACGCCCTTTCTGCCCCCAAGC	1264
2315	QY	AGGTTCTGCCCCCAGAGGGGCTGAGGCCCCACCCAGCAGTTGCCCCATGCCCTCTTG	2374
1265	DB	AGGTTCTGCCCCCAGAGGGGCTGAGGCCCCACCCAGCAGTTGCCCCATGCCCTCTTG	1324
2375	QY	GCTCCTTCCTTCAGGATCTTTCAGAGAGGCCCCCTTAGTACCTCTAAGGCCCTTCTTGG	2434
1325	DB	GCTCCTTCCTTCAGGATCTTTCAGAGAGGCCCCCTTAGTACCTCTAAGGCCCTTCTTGG	1384
2435	QY	GACAGCCCCAGGACCCCTTGCCCCCTGCGAAAGCAAGCCCCCACTTGAATCTTAAAGTGG	2494

1385	Db		GACAGCCCCAGGCA	CCCCCTCCCTCCCAAGCAAGCCCCCACTTGAC	TCTAAGATGG	1444	
2495	Qy		GGCTTGGAGACAT	CTCTCTTCTCTGGAGGCCAAACCCGGCCCTTGCA	TAGTTCCCAAGGT	2554	
1445	Db		GGCTTGGAGACAT	CTCTCTTCTCTGGAGGCCAAACCCGGCCCTTGCA	TAGTTCCCAAGGT	1504	
2555	Qy		CAGCTCCAGGCGAGCT	CTTCCCAAGTGAGCTCCCTCAGGTGGGTCTCT	CCACAGTGG	2614	
1505	Db		CAGCTCCAGGCGAGCT	CTTCCCAAGTGAGCTCCCTCAGGTGGGTCTCT	CCACAGTGG	1564	
2615	Qy		GCACAGACCTTGG	CCCCCTCTTGATCGGAGGCTGGACCCAGAGAGCT	TGAGATCTGT	2674	
1565	Db		GCACAGACCTTGG	CCCCCTCTTGATCGGAGGCTGGACCCAGAGAGCT	TGAGATCTGT	1624	
2675	Qy		CGAGCTCCACAC	CCACTTGCAGCGGCTCAGGAACAGGTGACCAT	GCGCAAGTTCTCCC	2734	
1625	Db		CGAGCTCCACAC	CCACTTGCAGCGGCTCAGGAACAGGTGACCAT	GCGCAAGTTCTCCC	1684	
2735	Qy		TGGTGTGCGGGGGT	TACGACGCGTGTGCTATGGA	CCCTTTTGGTGGAG	2794	
1685	Db		TGGTGTGCGGGGGT	TACGACGCGTGTGCTATGGA	CCCTTTTGGTGGAG	1744	
2795	Qy		ATGCAGGGGGCAT	TGCTGGGCGAGGGGCCATGTGGCGCAGGATAG	CTTGGGCTGTGCCC	2854	
1745	Db		ATGCAGGGGGCAT	TGCTGGGCGAGGGGCCATGTGGCGCAGGATAG	CTTGGGCTGTGCCC	1804	
2855	Qy		AGTCGAGGAGGAG	GACGAGGAGGCGAGGCTGAGTCCAGTCGAGAGAG	CAGCAGG	2914	
1805	Db		AGTCGAGGAGGAG	GACGAGGAGGCGAGGCTGAGTCCAGTCGAGAGAG	CAGCAGG	1864	
2915	Qy		AGGCGAGGGCTG	GAGAGCCACTGCCCAGGTCAGTGCAAGGCTGTG	CCTCAGGTCGGCA	2974	
1865	Db		AGGCGAGGGCTG	GAGAGCCACTGCCCAGGTCAGTGCAAGGCTGTG	CCTCAGGTCGGCA	1924	
2975	Qy		GGGTCTCCAC	CAGAGGCTCTCAGAGGCCACCCCATGTGGAGGAC	CATGGGCGAGTCTCCC	3034	
1925	Db		GGGTCTCCAC	CAGAGGCTCTCAGAGGCCACCCCATGTGGAGGAC	CATGGGCGAGTCTCCC	1984	
3035	Qy		TGGTCAGATCCG	GCACCTGTGTCAGTGATCGGAGGCGGCGCACAA	TATCTCCCTGGACA	3094	
1985	Db		TGGTCAGATCCG	GCACCTGTGTCAGTGATCGGAGGCGGCGCACAA	TATCTCCCTGGACA	2044	
3095	Qy		TTTCCGAGGTGGA	CCCCCGCTTACCTCAACCTCTCAGACCTGTAG	CGATATCAAGTACCTCC	3154	
2045	Db		TTTCCGAGGTGGA	CCCCCGCTTACCTCAACCTCTCAGACCTGTAG	CGATATCAAGTACCTCC	2104	
3155	Qy		CATTGAGTTTAT	GATCTTTCAGGAAATGCCCAAGTCGCTCAGCC	AGAGCGCCCTCCC	3214	
2105	Db		CATTGAGTTTAT	GATCTTTCAGGAAATGCCCAAGTCGCTCAGCC	AGAGCGCCCTCCC	2164	
3215	Qy		CCATGGCTGAGG	AGGAGCTGCGCAGTTCGCGAGCCACGTGGCCT	TGGCCAGGTGAAC	3274	
2245	Db		CCATGGCTGAGG	AGGAGCTGCGCAGTTCGCGAGCCACGTGGCCT	TGGCCAGGTGAAC	2224	
3275	Qy		TGGGCCCCCAG	CGAGGCTGAGATCA	CAGAGGAGTCAGAGGATGTGGA	CGCGTGTGG	3334
2225	Db		TGGGCCCCCAG	CGAGGCTGAGATCA	CAGAGGAGTCAGAGGATGTGGA	CGCGTGTGG	2284
3335	Qy		CAGAGGCTGCG	TGGCGAGGAGGCGAGTGCTCCTCGCGT	CACGAGCCTCTTCCACT	3394	
2285	Db		CAGAGGCTGCG	TGGCGAGGAGGCGAGTGCTCCTCGCGT	CACGAGCCTCTTCCACT	2344	
3395	Qy		TCCCTGGAGAG	CACTGCGCTGGATCAGCTGAGGCTGGGGCT	CGCTGAGAGATGA	3454	
2345	Db		TCCCTGGAGAG	CACTGCGCTGGATCAGCTGAGGCTGGGGCT	CGCTGAGAGATGA	2404	
3455	Qy		AGGCTCCGTGG	AGCACATCTCCGGATCTTGAAGGCGAGCCG	GAAGGCTGAGAGAGG	3514	
2405	Db		AGGCTCCGTGG	AGCACATCTCCGGATCTTGAAGGCGAGCCG	GAAGGCTGAGAGAGG	2464	
3515	Qy		AGGGCCCCC	CAGGAAAGCCAGGCTTGCTCTCTCCGCT	CTCAGGCTGAAGAGCT	3574	

2465 AGGGGCCCCCAGGAGGAGCCAGGCTTGTCTCTTTCGGCTCTCAGGTCTTGAAGAGCT 2524 Db
3575 GGGACCGAGCGCCGACATTCCTTAGGAGCTCTCAGATGAGCTGTGGTCTCTGGGCCAGT 3634 QY
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3635 CAGTGACACTGGCTTGCAGAGTGTGACGCCAGCTGCCCAGGCCACTGAGCAAAAG 3694 QY
2585 CAGTGACACTGGCTTGCAGAGTGTGACGCCAGCTGCCCAGGCCACTGAGCAAAAG 2644 Db
3695 ACGAGCGCCCTTGGAGAGCAGAGCGGTGTCTCATCTCTGCAACCTCAAGACTTCC 3754 QY
2645 ACGAGCGCCCTTGGAGAGCAGAGCGGTGTCTCATCTCTGCAACCTCAAGACTTCC 2704 Db
3755 AGCTTCTGACCATCTGCTGGTGGTGGCTGAGGACCTGGGTGTGTACACCTGAGCGTGA 3814 QY
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3815 GCAATGCGCTGGGACAGTGAACACACCGCGCTCTCCGAGGAGCAGAGCGCCCTCAT 3874 QY
2765 GCAATGCGCTGGGACAGTGAACACACCGCGCTCTCCGAGGAGCAGAGCGCCCTCAT 2824 Db
3875 CTTGCGCATGCCGATATCGGAGGTGTACGGGATGGGGTGTCTGCTGTGGGAGC 3934 QY
2825 CTTGCGCATGCCGATATCGGAGGTGTACGGGATGGGGTGTCTGCTGTGGGAGC 2884 Db
3935 CCGTGGAACTCTACGGCCCTGTGACCTACATGTGCAAGTGTGAGCGAGCGGCGAGCT 3994 QY
2885 CCGTGGAACTCTACGGCCCTGTGACCTACATGTGCAAGTGTGAGCGAGCGGCGAGCT 2944 Db
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4115 GCGCTCGAGCAAGTCTCTTGGAGGCGCCAGCCAGCTGGCTCTGAGGAGGAGGCC 4174 QY
3065 GCGCTCGAGCAAGTCTCTTGGAGGCGCCAGCCAGCTGGCTCTGAGGAGGAGGCC 3124 Db
4175 AGGGGCGGTACGCCCAACCCCTGCCAGCACAAGACCTTGGCATTTCCAGACACAGATCC 4234 QY
3125 AGGGGCGGTACGCCCAACCCCTGCCAGCACAAGACCTTGGCATTTCCAGACACAGATCC 3184 Db
4235 AGAGGGGCGGTACGCCCAACCCCTGCCAGCACAAGACCTTGGCATTTCCAGACACAGATCC 4294 QY
3185 AGAGGGGCGGTACGCCCAACCCCTGCCAGCACAAGACCTTGGCATTTCCAGACACAGATCC 3244 Db
4295 CCGCAAGATCATCCCTACACCCAGGACAGACAGCAGTGTGCGCGCAATACAGAGG 4354 QY
3245 CCGCAAGATCATCCCTACACCCAGGACAGACAGCAGTGTGCGCGCAATACAGAGG 3304 Db
4355 CCCTCAAGGGCCTGCGCCACCCGCAACCTGGCCAGCTGTGCGCGCAATACAGAGG 4414 QY
3305 CCCTCAAGGGCCTGCGCCACCCGCAACCTGGCCAGCTGTGCGCGCAATACAGAGG 3364 Db
4415 GGCACCTGTGTCTATCTTGGAGCTGTGCTTGGGCGCGAGCTGTCCCTGCGTGGCGG 4474 QY
3365 GGCACCTGTGTCTATCTTGGAGCTGTGCTTGGGCGCGAGCTGTCCCTGCGTGGCGG 3424 Db
4475 AGAGGGCCTCTACTCAGAACTGAGGTGAAGGACTTACCTGTGGCAGATGTGTAGTGCA 4534 QY
3425 AGAGGGCCTCTACTCAGAACTGAGGTGAAGGACTTACCTGTGGCAGATGTGTAGTGCA 3484 Db
4535 CCAGTACTGTGACAAACAGCAGCATCTGCACTGGACCTGGAGTCCGAGACATGATCA 4594 QY
3485 CCAGTACTGTGACAAACAGCAGCATCTGCACTGGAGTCCGAGACATGATCA 3544 Db
4595 TCACCGAAATACACCTGCTCAAGTGTGTGAGCTGGGCAATGACAGAGCCTTCAGCCAGG 4654 QY
3545 TCACCGAAATACACCTGCTCAAGTGTGTGAGCTGGGCAATGACAGAGCCTTCAGCCAGG 3604 Db

4655 AGAAGGTGCTGCCCTCAGACCAAGTTCAAGGACTACCTAGAGACCATGCTCCAGAGCTCC 4714 QY
3605 AGAAGGTGCTGCCCTCAGACCAAGTTCAAGGACTACCTAGAGACCATGCTCCAGAGCTCC 3664 Db
4715 TGGAGGGCCAGGGGCTGTCCACAGACAGACATCTGGGCCATCTGGTGTGACAGCCTTCA 4774 QY
3665 TGGAGGGCCAGGGGCTGTTCACACAGACATCTGGGCCATCTGGTGTGACAGCCTTCA 3724 Db
4775 TCATCTGAGCGCCAGTACCCGGTGTGACGAGGGTGTGACGCGACCTGACAGAGGAC 4834 QY
3725 TCATCTGAGCGCCAGTACCCGGTGTGACGAGGGTGTGACGCGACCTGACAGAGGAC 3784 Db
4835 TCGCAAGGGGCTGTCTCGGCTGTGAGCGCTGTCTAGCGGGGCTGTCCGGGGCGCGTGG 4894 QY
3785 TCGCAAGGGGCTGTCTCGGCTGTGAGCGCTGTCTAGCGGGGCTGTCCGGGGCGCGTGG 3844 Db
4895 CTTTCTGCGACGACACTCTGTGCGCCCGAGCCCTGGGGCGCGCCCTGCGCTCCAGTGGC 4954 QY
3845 CTTTCTGCGACGACACTCTGTGCGCCCGAGCCCTGGGGCGCGCCCTGCGCTCCAGTGGC 3904 Db
4955 TGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCTGTTCGGGGCGCGCCCGTGGACCT 5014 QY
3905 TGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCTGTTCGGGGCGCGCCCGTGGACCT 3964 Db
5015 TCCTTACCGCGCGCTGTGCGCTCTTTCGTGCGCAATCGCGAGAGAGAGCGCGCTGCTGT 5074 QY
3965 TCCTTACCGCGCGCTGTGCGCTCTTTCGTGCGCAATCGCGAGAGAGAGCGCGCTGCTGT 4024 Db
5075 ACAAGAGGACAACTTGGGCCAGGTGCGCTGAGGTGCGGCCCGCCAGACACCTTGGTCTC 5134 QY
4025 ACAAGAGGACAACTTGGGCCAGGTGCGCTGAGGTGCGGCCCGCCAGACACCTTGGTCTC 4084 Db
5135 CCGCTGGGGGTGCTGTGACAGCGCGCAATAAAAAAGCAGCCGCGGAGAAAAAAA 5194 QY
4085 CCGCTGGGGGTGCTGTGACAGCGCGCAATAAAAAAGCAGCCGCGGAGAAAAAAA 4144 Db
5195 AAAAAA 5207 QY
4145 AAAAAA 4157 Db

RESULT 13
US-10-311-034-46
Sequence 46, Application US/10311034
Publication No. US20040023242A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAU, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BOROMSKY, Mark L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Yan
APPLICANT: GANDHI, Ameena R.
APPLICANT: TRIBOULEX, Catherine M.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: YAO, Monique G.
APPLICANT: LU, Dyung Aina M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: RAMKUMAR, Javalaxmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Damiel B.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAFALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: LO, Terence P.

[illegible]

2578	QA	CAAGTGA	CTCCCTCAGGGTGGGCTCTCCAGGTGGGCA	CAGAGCTGGGCCCTCGTG	2637	
613	DB	CAAGTGA	CTCCCTCAGGGTGGGCTCTCCAGGTGGGCA	CAGAGCTGGGCCCTCGTG	672	
2638	QA	GATCGGAGGGCTG	GACCCAGAGGCTGAGATCTGTCGACTCCA	CCACACCTTGCAG	2697	
673	DB	GATCGGAGGGCTG	GACCCAGAGGCTGAGATCTGTCGACTCCA	CCACACCTTGCAG	732	
2698	QA	CGGCTCAGGACAGT	GACCATGGCAGATTCTCCCTGGTGGT	CGGGGGGTACGCA	2757	
733	DB	CGGCTCAGGACAGT	GACCATGGCAGATTCTCCCTGGTGGT	CGGGGGGTACGCA	792	
2758	QA	GGCGTGGCTGTAT	GGCACCTTTGCCCTTTGGTGGAGATG	CAGGGGCGATGCTGGGCGAG	2817	
793	DB	GGCGTGGCTGTAT	GGCACCTTTGCCCTTTGGTGGAGATG	CAGGGGCGATGCTGGGCGAG	852	
2818	QA	GGGCCCCATGTGGG	CCAGGATAGCTGGGCTGTGTCACGTCGGAGGAGG	AGGAGCAGGAG	2877	
853	DB	GGGCCCCATGTGGG	CCAGGATAGCTGGGCTGTGTCACGTCGGAGGAGG	AGGAGCAGGAG	912	
2878	QA	GAGGCCAGGGCTG	ATCCAGTTCGGAGGACGACGAGGCCAGGGCT	GTAGAGCCACTG	2937	
913	DB	GAGGCCAGGGCTG	ATCCAGTTCGGAGGACGACGAGGCCAGGGCT	GTAGAGCCACTG	972	
2938	QA	CCCCAGGTCACTG	CAAGGCCCTGCTCCCTGAGGTCCG	CAGGGCTCCAC	CAGGAGCTCTCCA	2997
973	DB	CCCCAGGTCACTG	CAAGGCCCTGCTCCCTGAGGTCCG	CAGGGCTCCAC	CAGGAGCTCTCCA	1032
2998	QA	GAGCCACCCATGGG	AGGACATCGGCAGAGTCTCCCTGGTGGAGATC	CGGGACCTGTCA	3057	
1033	DB	GAGCCACCCATGGG	AGGACATCGGCAGAGTCTCCCTGGTGGAGATC	CGGGACCTGTCA	1092	
3058	QA	GGTGATCGGAGGCGG	CGGACACAAATATCCCTGGACATTTCCGAGGTG	ACCCGGCTAC	3117	
1093	DB	GGTGATCGGAGGCGG	CGGACACAAATATCCCTGGACATTTCCGAGGTG	ACCCGGCTAC	1152	
3118	QA	CTCAACCTCTCAG	ACCTGTATCAAGTATCCTCCATTCAGTATTATG	ATCTTCAGG	3177	
1153	DB	CTCAACCTCTCAG	ACCTGTATCAAGTATCCTCCATTCAGTATTATG	ATCTTCAGG	1212	
3178	QA	AAAGTCCCAAGTCCG	CTCAGCAGAGCCGCTCCCCATGCTGAGGAGG	AGCTGGCC	3237	
1213	DB	AAAGTCCCAAGTCCG	CTCAGCAGAGCCGCTCCCCATGCTGAGGAGG	AGCTGGCC	1272	
3238	QA	GAGTCCCGAGGCC	ACGCTGGCCCTGGCCAGAGTGAACTGGGCCCC	CCACCGCAGGCTGGAG	3297	
1273	DB	GAGTCCCGAGGCC	ACGCTGGCCCTGGCCAGAGTGAACTGGGCCCC	CCACCGCAGGCTGGAG	1332	
3298	QA	ATCAGAGGAGT	CAGAGGATGGAGCGGCTGCTGGCAGAGGCTG	CCGTGGGCAGGAG	3357	
1333	DB	ATCAGAGGAGT	CAGAGGATGGAGCGGCTGCTGGCAGAGGCTG	CCGTGGGCAGGAG	1392	
3358	QA	CGCAAGTGTCTCG	CGCTCAGCGAGCTCTTCCATCTCCCTGGGAGG	ACCTGCCGCTG	3417	
1393	DB	CGCAAGTGTCTCG	CGCTCAGCGAGCTCTTCCATCTCCCTGGGAGG	ACCTGCCGCTG	1452	
3418	QA	GATGAGCTCTCAG	AGCTGGGCTGCTGTGAGAGTGAAGGCTTC	CGTGGAGCACTCTCC	3477	
1453	DB	GATGAGCTCTCAG	AGCTGGGCTGCTGTGAGAGTGAAGGCTTC	CGTGGAGCACTCTCC	1512	
3478	QA	CGGATCTGAAGG	CGACCGGAGGTTCTGGAGAGGAGGGGCCCC	CCACAGGAAGACCA	3537	
1513	DB	CGGATCTGAAGG	CGACCGGAGGTTCTGGAGAGGAGGGGCCCC	CCACAGGAAGACCA	1572	
3538	QA	GGCCTCTCTTC	CGGCTCTCAGGCTGTGAAGCTGGACCGAGCG	CCGACATTCCTA	3597	
1573	DB	GGCCTCTCTTC	CGGCTCTCTCAGGCTGTGAAGCTGGACCGAGCG	CCGACATTCCTA	1632	
3598	QA	AGGAGCTCTCAG	ATGAGACTGTGGTCTTGGGCCAGTCA	GTGATGACTGTGGCTCTCCAGGTTG	3657	
1633	DB	AGGAGCTCTCAG	ATGAGACTGTGGTCTTGGGCCAGTCA	GTGATGACTGTGGCTCTCCAGGTTG	1692	
3658	QA	TCAGCCAGCAG	CTGCCAGGCCCACTGGAGCAAGA	CGGAGCCCTCTGGAGAGCAGC	3717	

Db	1693	TCAGCCACGACAGCTGCCACGACCACTGAGGCAAGACGAGACCCCTCTGGAGGACG	1752
QY	3718	AGCGTGCTCTCATCTCTGCCACCCCTCAGAACTTCCAGCTTCTGACCATCTCTGGTGGTG	3777
Db	1753	AGCGGTGCTCATCTCTGCCACCCCTCAGAACTTCCAGCTTCTGACCATCTCTGGTGGTG	1812
QY	3778	GTGGCTGAGGACCTGGGTGTATACCTGACGCGTGAGCAATGCGCTGGGACAGTAGTACC	3837
Db	1813	GTGGCTGAGGACCTGGGTGTATACCTGACGCGTGAGCAATGCGCTGGGACAGTAGTACC	1872
QY	3838	ACCACGGCGTCTCCCGAAGGACAGCGCCCTCATCTTTGGCCATGCCCGATATCCGG	3897
Db	1873	ACCACGGCGTCTCCCGAAGGACAGCGCCCTCATCTTTGGCCATGCCCGATATCCGG	1932
QY	3898	GAGTGATACGGGATGGGTGCTGCTGTGTGAAGCCCGTGAATTCCTACGGCCCTGTG	3957
Db	1933	GAGTGATACGGGATGGGTGCTGCTGTGTGAAGCCCGTGAATTCCTACGGCCCTGTG	1992
QY	3958	ACCTACATTGTGCACTGACGCTAGAAAGCGGACGTGGAACAACATGGCCTCCGACATC	4017
Db	1993	ACCTACATTGTGCACTGACGCTAGAAAGCGGACGTGGAACAACATGGCCTCCGACATC	2052
QY	4018	TTTGACTCTCTACTACGTACCAAGCAAGCTCTCCCGGGTGGCACTTACCTTCCGACAG	4077
Db	2053	TTTGACTCTCTACTACGTACCAAGCAAGCTCTCCCGGGTGGCACTTACCTTCCGACAG	2112
QY	4078	GCATGTGCACGAAGGACGAATGGGTCCCTACAGACGCCCTCGGACAAAGTCTCTCTG	4137
Db	2113	GCATGTGTACGAAGGACGAATGGGTCCCTACAGACGCCCTCGGACAAAGTCTCTCTG	2172
QY	4138	GGAGGGCCACCCACTGGGCTCTGAGGAGGAGACCAAGGGCGGTGAGCCCAACCCCTG	4197
Db	2173	GGAGGGCCACCCACTGGGCTCTGAGGAGGAGACCAAGGGCGGTGAGCCCAACCCCTG	2232
QY	4198	CCGACACAAAGACCTTGCATTTCCAGACACAGATCCAGAGGGCGCGTTCAGGTGGTG	4257
Db	2233	CCGACACAAAGACCTTGCATTTCCAGACACAGATCCAGAGGGCGCGTTCAGGTGGTG	2292
QY	4258	CGCCAAATGCTGGGAGAAAGCCAGCGGGCGGGCGCTGGCGGCAAGATCATCCCTACCAAC	4317
Db	2293	CGCCAAATGCTGGGAGAAAGCCAGCGGGCGGGCGCTGGCGGCAAGATCATCCCTACCAAC	2352
QY	4318	CCCAAGGACAGACAGACAGTGTGCGCGAATACGAGGCGCTTCAAGGCGCTGGCGCACCCG	4377
Db	2353	CCCAAGGACAGACAGACAGTGTGCGCGAATACGAGGCGCTTCAAGGCGCTGGCGCACCCG	2412
QY	4378	CACCTGGCCACGTGACGAGCCTTACTCAGGCCCGCGCACCTGTGTCTCATCTTGGAG	4437
Db	2413	CACCTGGCCACGTGACGAGCCTTACTCAGGCCCGCGCACCTGTGTCTCATCTTGGAG	2472
QY	4438	CTGTGCTCTGGGCCCGACGTGCTCCCTGCTGGCGGAGAGGGCGCTCCTACTCAGAAATCT	4497
Db	2473	CTGTGCTCTGGGCCCGACGTGCTCCCTGCTGGCGGAGAGGGCGCTCCTACTCAGAAATCT	2532
QY	4498	GAGGTGAAGNACTACTGTGTGGGAGATGTTGAGTGGCACCCGAGTACCTGCACACAGACAC	4557
Db	2533	GAGGTGAAGNACTACTGTGTGGGAGATGTTGAGTGGCACCCGAGTACCTGCACACAGACAC	2592
QY	4558	ATCTTGCACTTGGACCTGGAGTCCGAGAAATGATCATCACCGGAATACAACTGCTCAAG	4617
Db	2593	ATCTTGCACTTGGACCTGGAGTCCGAGAAATGATCATCACCGGAATACAACTGCTCAAG	2652
QY	4618	GTCTGTGACCTGGGCAATGCACAGACCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAG	4677
Db	2653	GTCTGTGACCTGGGCAATGCACAGACCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAG	2712
QY	4678	TTCAGGACTACCTAGAGACCATGGCTCAGAGCTCTTGGAGGGCCAGGGGGCTGTTCAC	4737
Db	2713	TTCAGGACTACCTAGAGACCATGGCTCAGAGCTCTTGGAGGGCCAGGGGGCTGTTCAC	2772
QY	4738	CAGACAGACATCTGGGCCATTCGGTGTGACAGCCTTTCATCATGCTGAGCGCCGAGTACC	4797

2773	DB	CAGACAGACATCTGGGCGCATCGGTGTGACAGCCTTTCATCATGCTGAGCGCGCGAGTACCGG	28332
4758	QY	GTGAGCAGCAGAGGGTGCACGCGACCTGCAGAGAGAGACTGCGCAAGAGGGCTGTCCTCGGCTG	4857
2833	DB	GTGAGCAGCAGAGGGTGCACGCGACCTGCAGAGAGAGACTGCGCAAGAGGGCTGTCCTCGGCTG	2892
4858	QY	AGCCGCTGCTACGCGGGGTGTTCGCGGGGCGCGCTTGCGCTTCCTGCGCAGCAGCTCTGTGC	4917
2893	DB	AGCCGCTGCTACGCGGGGTGTTCGCGGGGCGCGCTTGCGCTTCCTGCGCAGCAGCTCTGTGC	2952
4918	QY	GCCCAGCCCTGGGGCGCGCCCTCGCGCTGCAGCTGCCTGCAGTGCCCTGGCTAAACAGAG	4977
2953	DB	GCCCAGCCCTGGGGCGCGCCCTCGCGCTGCAGCTGCCTGCAGTGCCCTGGCTAAACAGAG	3012
4978	QY	GAGGGCCGCGCTTTCGCGGCGCGCGCGCTGACCTTCCCTACCGCGCGGCTGCGGCTC	5037
3013	DB	GAGGGCCGCGCTTTCGCGGCGCGCGCGCTGACCTTCCCTACCGCGCGGCTGCGGCTC	3072
5038	QY	TTCGTGCAGCAATCGCAGAAAGAGACGCGCTGCTGTACAGAGGGACACACCTGGGCCAG	5097
3073	DB	TTCGTGCAGCAATCGCAGAAAGAGACGCGCTGCTGTACAGAGGGACACACCTGGGCCAG	3132
5098	QY	GTGCGCTGAGGGTCGCGCGGCGCACACCTTGTGCTCCCGCTGGGGGCTCGCTGCAGAGC	5157
3133	DB	GTGCGCTGAGGGTCGCGCGGCGCACACCTTGTGCTCCCGCTGGGGGCTCGCTGCAGAGC	3192
5158	QY	CGCCAAATAAAGCGCAGCCGCGGAGAAAA	5190
3193	DB	CGCCAAATAAAGCGCAGCCGCGGAGAAAA	3225

RESULT 14

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US-10-425-114-26278
; Sequence 26278, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Tongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26278
; LENGTH: 1235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI
US-10-425-114-26278

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Query Match	24.0%;	Score 1251.4;	DB 13;	Length 1253;
Best Local Similarity	99.9%;	Pred. No. 1.5e-297;		
Matches 1252;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
3933	GCCTGGGAATCCTACGGCCCTGTGACCTACATTGCGAGTGAGCTGAAGCGCGCAG	3992		
Ddb	1 GCCTGGGAATCCTACGGCCCTGTGACCTACATTGCGAGTGAGCTGAAGCGCGCAG	60		
3993	CTGGACCACTGGCCCTCGACATCTTTGACTGTGCTACTGACGAGCAAGCTCTCCCG	4052		
Ddb	61 CTGGACCACTGGCCCTCGACATCTTTGACTGTGCTACTGACGAGCAAGCTCTCCCG	120		
4053	GGGTGCACCTACACCTTCCGACGGCATGTGTGACGAGCAGGAATGGTCCCTACAG	4112		
Ddb	121 GGGTGCACCTACACCTTCCGACGGCATGTGTGACGAGCAGGAATGGTCCCTACAG	180		
4113	CAGCCCTCTGGAGCAAGTCTCTCTGGAGGGCCACAGCCACTGSGCTCTGAGGAGGAG	4172		

Db 181 CAGCCCTCGGAGCAAGTCTCTCTGGAGGGCCAGCCACCTTGGGCTCTGAGGAGAG 240
QY 4173 CAGGGGCGGTGAGCCCAACCCCTGCGCCAGCAAAAGACCTTCGATTCACAGACACAGAT 4232
Db 241 CAGGGGCGGTGAGCCCAACCCCTGCGCCAGCAAAAGACCTTCGATTCACAGACACAGAT 300
QY 4233 CAGAGGGGCGGTGAGCGGTGAGCGCAATGCTGGAGAAAGCCAGCGGGCGGCGCT 4292
Db 301 CAGAGGGGCGGTGAGCGGTGAGCGCAATGCTGGAGAAAGCCAGCGGGCGGCGCT 360
QY 4293 GGGCGGCAAGATCATCCCTTACCACCCCAAGACAGACAGAGTGTGCGCGCAATACGA 4352
Db 361 GGGCGGCAAGATCATCCCTTACCACCCCAAGACAGACAGAGTGTGCGCGCAATACGA 420
QY 4353 GGGCGGCAAGATCATCCCTTACCACCCCAAGACAGACAGAGTGTGCGCGCAATACGA 4412
Db 421 GGGCGGCAAGATCATCCCTTACCACCCCAAGACAGACAGAGTGTGCGCGCAATACGA 480
QY 4413 CCGGCACTGCTGCTCATCTTGGAGTGTGCTGCTGGGCGGAGCTGCTCCCTGCTGGC 4472
Db 481 CCGGCACTGCTGCTCATCTTGGAGTGTGCTGCTGGGCGGAGCTGCTCCCTGCTGGC 540
QY 4473 CGAGAGGGCTCTTACTCAGATCTGAGTGAAGACTTACCTGTGGAGATGTTGAGTGC 4532
Db 541 CGAGAGGGCTCTTACTCAGATCTGAGTGAAGACTTACCTGTGGAGATGTTGAGTGC 600
QY 4533 CACCCAGTACTGACCAACCCAGCACATCTCTGACCTGAGCTGAGTCCGAGAACATGAT 4592
Db 601 CACCCAGTACTGACCAACCCAGCACATCTCTGACCTGAGCTGAGTCCGAGAACATGAT 660
QY 4593 CACCCAGTACTGACCAACCCAGCACATCTCTGACCTGAGCTGAGTCCGAGAACATGAT 4652
Db 661 CACCCAGTACTGACCAACCCAGCACATCTCTGACCTGAGCTGAGTCCGAGAACATGAT 720
QY 4653 GGAAGAGTGTCTGCTCAGACCAAGTTCAAGGACTTACCTAGAGACCATGGCTCCAGAGCT 4712
Db 721 GGAAGAGTGTCTGCTCAGACCAAGTTCAAGGACTTACCTAGAGACCATGGCTCCAGAGCT 780
QY 4713 CCGGAGGGCCAGGGGCTGTTCCACAGACACATCTGGGCTCGGTGTGACAGGCTT 4772
Db 781 CCGGAGGGCCAGGGGCTGTTCCACAGACACATCTGGGCTCGGTGTGACAGGCTT 840
QY 4773 CATCATGCTGAGCGCGAGTACCCTGAGCAGCGAGGCTGACCGGACCTGACAGAGG 4832
Db 841 CATCATGCTGAGCGCGAGTACCCTGAGCAGCGAGGCTGACCGGACCTGACAGAGG 900
QY 4833 ACTGCGCAAGGCTGCTGGGCTGAGCGGCTGCTACGGGGGCTGTCCGGGGGCGGCT 4892
Db 901 ACTGCGCAAGGCTGCTGGGCTGAGCGGCTGCTACGGGGGCTGTCCGGGGGCGGCT 960
QY 4893 GGCCTTCTGCGCAGACCTGTGCGCCAGCCCTGGGGCGGCTGCTGCGGCTCCAGCTG 4952
Db 961 GGCCTTCTGCGCAGACCTGTGCGCCAGCCCTGGGGCGGCTGCTGCGGCTCCAGCTG 1020
QY 4953 CTTGCAAGTGGGCTTACAGAGAGGGCCGGGCTGTTCCGGGCGGCGGCTGAC 5012
Db 1021 CTTGCAAGTGGGCTTACAGAGAGGGCCGGGCTGTTCCGGGCGGCGGCTGAC 1080
QY 5013 CTTCCCTTACCGCGGCTGCGGCTCTTCTGCGCAATGCGAGAGAGACGCGGCTGCT 5072
Db 1081 CTTCCCTTACCGCGGCTGCGGCTCTTCTGCGCAATGCGAGAGAGACGCGGCTGCT 1140
QY 5073 GTACAGAGGCAACCTGGGCGGCTGCGGCTGAGGCTGCGGCGGCGGCTGCTGCTGCT 5132
Db 1141 GTACAGAGGCAACCTGGGCGGCTGCGGCTGAGGCTGCGGCGGCGGCTGCTGCTGCT 1200
QY 5133 TCCCGGCTGGGGTCTGCTGACAGCGGCCAATAAAGGACGACAGCGGGCGAG 5185
Db 1201 TCCCGGCTGGGGTCTGCTGACAGCGGCCAATAAAGGACGACAGCGGGCGAG 1253

RESULT 15

US-09-864-408A-8947
; Sequence 8947, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkete, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864.408A
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; NUMBER OF SEQ ID NOS: 2000-05-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8947
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(1)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-09-864-408A-8947

Query Match 6.9%; Score 358.4; DB 11; Length 382;
Best Local Similarity 99.7%; Pred. No. 4.2e-78;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 502 GGTGCGCCAGGTGCTCTGCAAGSCAGAGCTGCTGTGCTTGGGGGGGCAATGAGCCGGAC 561
Db 13 GGTGCGCCAGGTGCTCTGCAAGSCAGAGCTGCTGTGCTTGGGGGGGCAATGAGCCGGAC 72
QY 562 TCAGAGAGCAAGCAAGCCAGCGGAGGAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATT 621
Db 73 TCAAGAGCAAGCAAGCCAGCGGAGGAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATT 132
QY 622 GGAAGGGGCGTGTGGGCTTCTGTAAGAGAGTGCAGACAAAGGAAACAAAGATCTTGTGC 681
Db 133 GGAAGGGGCGTGTGGGCTTCTGTAAGAGAGTGCAGACAAAGGAAACAAAGATCTTGTGC 192
QY 682 GCTGCCAAGTTCATCCCTTACGAGAGCAAGAACTCGGGCCCGAGCATACAGGAGCCGAGAC 741
Db 193 GCTGCCAAGTTCATCCCTTACGAGAGCAAGAACTCGGGCCCGAGCATACAGGAGCCGAGAC 252
QY 742 ATCTTGGCGCGGCTGAGCCACCCCTGCTCACGGGGGCTGTGGACCAAGTTTGAGACCCGC 801
Db 253 ATCTTGGCGCGGCTGAGCCACCCCTGCTCACGGGGGCTGTGGACCAAGTTTGAGACCCGC 312
QY 802 AAGACCTTCATCTCTGAGCTGTGCTCATCCGAGAGCTGTCTGGACCCGCTGTAC 861
Db 313 AAGACCTTCATCTCTGAGCTGTGCTCATCCGAGAGCTGTCTGGACCCGCTGTAC 372

Search completed: April 26, 2004, 18:26:10
Job time : 1377 secs

22-OCT-2001; 2001WO-US032616.
14-NOV-2000; 2000US-00711134.
17-MAY-2001; 2001US-00858664.
XX (PEKE) PE CORP NY.
XX Wei M, Ketchum K, Di Francesco V, Beasley EM;
XX WPI; 2002-500223/53.
XX P-PSDB; AAO15372.
XX New kinase proteins related to myosin light chain kinase subfamily and
XX encoding polynucleotide, useful for diagnosing, treating disease or
XX condition mediated by the kinase protein and for identifying modulators.
XX Claim 23; Fig 3; 96pp; English.
XX The invention comprises the amino acid and coding sequences (located on
XX chromosome 1) of a human kinase protein that is related to the myosin
XX light chain kinase subfamily. The human kinase DNA and protein sequences
XX of the invention are useful for identifying agents that modulate the
XX activity of the human kinase protein. Kinase-modulating agents are useful
XX for treating a disease or condition mediated by a human kinase protein.
XX The human kinase DNA sequences can be used to produce transgenic animals
XX which are useful for studying the function of kinase proteins and
XX identifying/evaluating modulators of kinase protein activity. The present
XX DNA sequence encodes the human kinase protein of the invention
XX
XX Sequence 5207 BP; 988 A; 1758 C; 1612 G; 849 T; 0 U; 0 Other;
Query Match 100.0%; Score 5207; DB 6; Length 5207;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCAGGAGAACTCCTCTGATCACTGGCCAGCTGAGGTGAGAGTGGAGAGGAGTG 60
DB 1 CAGCAGGAGAACTCCTCTGATCACTGGCCAGCTGAGGTGAGAGTGGAGAGGAGTG 60
QY 61 GTTCCATTAGAGAGTACTCTTAATCTGTCAGAGAGCTGGGGGTCAGAGTGGGTGCTGT 120
DB 61 GTTCCATTAGAGAGTACTCTTAATCTGTCAGAGAGCTGGGGGTCAGAGTGGGTGCTGT 120
QY 121 CGTTGGGCTGGGGGGGTGTTTCAGTTGCCACAGTGTATCTCAGAGGTCTTCAACCAACAT 180
DB 121 CGTTGGGCTGGGGGGGTGTTTCAGTTGCCACAGTGTATCTCAGAGGTCTTCAACCAACAT 180
QY 181 CCAAGCATGGTAGGCTGTGGTGGACCCAGGTTGTGTGCTGGGAGGTGTTCTCCAC 240
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QY 241 AGTTCCCTCCCTCCCTCCAGGGCCCCCATCCATGCAAGTAAACCATCGAGATGTGAG 300
DB 241 AGTTCCCTCCCTCCCTCCAGGGCCCCCATCCATGCAAGTAAACCATCGAGATGTGAG 300
QY 301 GCACAGAGGGGAGACGGCCCAATTCGAGGCTATCATTTAGGGGAGCCACAGCCCTCG 360
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QY 361 GTGACCTGTGTACAGGACAGCTCCAGTGTGGACAGCACCCGGCTTAGCCAGCAGCAA 420
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QY 421 GAAGGACACCATATCTCTGTGTGAGGCTATGAGGCTGAGAGTATGCGGGGTTTAC 480
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QY 541 GGGGGGGAACAATGAGCCGAGCTCAGAGAGCAAGCCACCGGAGAGAGTGCATCTCTTC 600
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DB 661 AAAGGAACAAGATCTTGTGGCTGCGCAAGTTTATCCCTCTACGAGAGCAACTCGGGCC 720
QY 721 CAGGCATACAGGAGGAGAGATCTTGGCCGCGCTGAGCCACCCGCTGCTGTCAGCGGGCTG 780
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QY 781 CTGAGCAGATTGAGACCCGAGAGCCCTCATCTCTATCTCTGAGAGTGTCTCATCCGAG 840
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DB 841 CAGCTGTGAGCCGCTGTATCAGGAAGGGGCTGTGATCGAGGAGCCGAGGTCAAGGCTCTAC 900
QY 901 ATCCAGAGCTGTGTGGAGGGGCTGCATCTCTCAGAGAGCCATCGGCTTCTCCACCTGGAC 960
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DB 1021 TTTGGCTTTGCCAGAAATCACCACCCAGCAGAGCTGAGTTCAGCCAGTACGCTCCCT 1080
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DB 1081 GAGTTCTGCTCTCCCGAGATCATCCAGAGAACCTCTGTGAGCGAAGCCCTCCGACATTTGG 1140
QY 1141 GCCATGGGTGTCATCTCTACCTCAGCTCAGCTGACCTGCTCATCCCATTTGCGCGGAGAGT 1200
DB 1141 GCCATGGGTGTCATCTCTACCTCAGCTCAGCTGACCTGCTCATCCCATTTGCGCGGAGAGT 1200
QY 1201 GACCGTGCACCCCTCTCTGAGGGGGCGGTGTCATGAGAGAGCCCATGCGT 1260
DB 1201 GACCGTGCACCCCTCTCTGAGGGGGCGGTGTCATGAGAGAGCCCATGCGT 1260
QY 1261 GCCACCTCAGGAGAGAGCCCAAGCTTCATCAAGGCTACGCTGAGAGAGCCCTCAG 1320
DB 1261 GCCACCTCAGGAGAGAGCCCAAGCTTCATCAAGGCTACGCTGAGAGAGCCCTCAG 1320
QY 1321 GCCCGGCTAGTGGCGCCAGTGCCTCTCCACCCCTGCTGCTGAAATCCATGCTCGG 1380
DB 1321 GCCCGGCTAGTGGCGCCAGTGCCTCTCCACCCCTGCTGCTGAAATCCATGCTCGG 1380
QY 1381 GAGGAGGCCACTTTCATCAACCAAGCAGCTCAAGTTCTCTGCGCCGAGTCTGCTG 1440
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QY 1441 CAGCGTTCCCTGATGAGTCAAGTCCATCTCTGAGTGGCTTCCATCTCTGAGTGTCTG 1500
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QY 1501 CGGGGCCACCCGAGAGCCCTCTCCGCGGTAGCCGCGACCTCTGCGAGGACACTGGT 1560
DB 1501 CGGGGCCACCCGAGAGCCCTCTCCGCGGTAGCCGCGACCTCTGCGAGGACACTGGT 1560
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1741 CGGCTGCACTCCGAGGGTCCGGGCCACCGGCCCGCCAGGGCTGCTGCCCGGCCAC 1800
1742 CGGCTGCACTCCGAGGGTCCGGGCCACCGGCCCGCCAGGGCTGCTGCCCGGCCAC 1800
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2221 CCATCCAGTGGTGGCCACCGGCCCGGGCGGCACTGTGAGAGCGCGCTACATT 2280
2222 CCATCCAGTGGTGGCCACCGGCCCGGGCGGCACTGTGAGAGCGCGCTACATT 2280
2281 TGGGGGAGAGCGGCCACCGGCCCGGGCGGCACTGTGAGAGCGCGCTACATT 2340
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2341 AGCCCGGAGAGCGGCCACCGGCCCGGGCGGCACTGTGAGAGCGCGCTACATT 2400
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3782 GCTGAG 3840
3841 ACGGGGCTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3900

Db	4921	CAGCCCTGGGGCGGGCCCTTGGCGGTCCAGCTGCTTGCAGTGCCTTGGCTAACAGAGGAG	4980
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Db	4981	GGCCCGGCGCTGTTCGGGCGCCCGCGCGGTGACCTTTCCTTACCGCGCGGTGCGCGTCTTC	5040
Qy	5041	GTGGGCAATCGCAGAGAGACGCGGCTGCTGTACAGAGACACAACTGGGCCCGAGTG	5100
Db	5041	GTGGGCAATCGCAGAGAGACGCGGCTGCTGTACAGAGACACAACTGGGCCCGAGTG	5100
Qy	5101	CGCTGAGGGTTCGGCCCGCGGCACACCCCTTGGTCTCCCGCTCGGGGTGCGTGACAGCGGC	5160
Db	5101	CGCTGAGGGTTCGGCCCGCGGCACACCCCTTGGTCTCCCGCTCGGGGTGCGTGACAGCGGC	5160
Qy	5161	CAATATAAAACGCACAGCGCGGCGAGAAAAAAGAAAAA	5207
Db	5161	CAATATAAAACGCACAGCGCGGCGAGAAAAAAGAAAAA	5207
RESULT 2			
AAL43908			
XX	ID	AAL43908 standard; DNA; 5207 BP.	
AC			
XX	AAL43908;		
DT	19-SEP-2002	(first entry)	
XX			
DE		Human kinase protein coding sequence 1.	
XX			
XX		Human; gene; ds; gene therapy; chromosome 1; kinase protein;	
KW		myosin light chain kinase subfamily; kinase protein-mediated disease;	
KW		transgenic animal.	
XX			
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	109..5106	
FT		/*tag= a	
FT		/product= "Human kinase protein"	
XX			
PN	WO200240683-A2.		
XX			
PD	23-MAY-2002.		
XX			
PF	22-OCT-2001; 2001WO-US032616.		
XX			
PR	14-NOV-2000; 2000US-00711134.		
PR	17-MAY-2001; 2001US-00858664.		
XX			
XX	(PEXE) PE CORP NY.		
PA			
XX			
PI	Wei M, Ketchum K, Di Francesco V, Beasley EM;		
XX			
DR	WPI; 2002-500223/53.		
XX	P-PSDB; AAO15372.		
DR			
XX			
PT	New kinase proteins related to myosin light chain kinase subfamily and		
PT	encoding polynucleotide, useful for diagnosing, treating disease or		
PT	condition mediated by the kinase protein and for identifying modulators.		
XX			
PS	Claim 23; Fig 1; 96pp; English.		
XX			
CC	The invention comprises the amino acid and coding sequences (located on		
CC	chromosome 1) of a human kinase protein that is related to the myosin		
CC	light chain kinase subfamily. The human kinase DNA and protein sequences		
CC	of the invention are useful for identifying agents that modulate the		
CC	activity of the human kinase protein. Kinase-modulating agents are useful		
CC	for treating a disease or condition mediated by a human kinase protein.		
CC	The human kinase DNA sequences can be used to produce transgenic animals		
CC	which are useful for studying the function of kinase proteins and		
CC	identifying/evaluating modulators of kinase protein activity. The present		
CC	DNA sequence encodes the human kinase protein of the invention		
XX			

5Q	Sequence	5207 BP; 988 A; 1758 C; 1612 G; 849 T; 0 U; 0 Other;
	Query Match	100.0%; Score 5207; DB 6; Length 5207;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 5207; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CAGCAGAGAACTCCTTCGTGATCACCTGCGCCAGCTGAGGTACAGATGGGAGAGGAGGAGTG 60
DB	1	
QY	61	GTTCATTGAAGGAGTACTCCTAACTGTCAAGAGCCTGGCGGTCAGGATGGGGGTGCTGT 120
DB	61	
QY	121	CGCTTGGGCTGGGGGGGTGTTGAGTTGCCCAAGTGTATCTCAGGGTCTCAACCAACCAT 180
DB	121	
QY	181	CCAAGCATGTTAGGCTGTGGCTGGCAACCCAGGGTGTGTGGCTGGGAGAGTGTCTCCAC 240
DB	181	
QY	241	AGTTCCCTCCCTGCCCCCTCCAGGGCCCCCATTCMATGACAGTAAACCATTCGAGGATGTGCAG 300
DB	241	
QY	301	GCACAGACAGGCGAAACGGCCCCAATTCGAGGCTATCATTCGAGGCGCACCCACAGCCCTCG 360
DB	301	
QY	361	GTGACCTGGTACAAGGACAGCGTCCAGTGGTGGACAGCACCCGGCTTACCCAGCAGCAA 420
DB	361	
QY	421	GAAGGCACCATACTCCCTGGTCTCAGGCATGTGGCCTCGAAGGATGCCGGGTTTAC 480
DB	421	
QY	481	ACCTGCCCTGGCCCCAAAACACTGGTGGCCAGGTGCTCTGCAAGCAGAGCTGCTGGTGCTT 540
DB	481	
QY	541	GGGGGGACAATGAGCCGGACTCAGAGAAGCAAGCCACCGGAGGAGCTGCATCCCTTC 600
DB	541	
QY	601	TATGAGGTCAAGGAGGAGATGGGAAGGGCGGTGTTGGCTTCGTAAAAAGATGCAGCAC 660
DB	601	
QY	661	AAAGGAAAACAAGATCTTGTGCGCTGCCAAGTTCTATCCCCCTACCGAGGAGAACTCGGGCC 720
DB	661	
QY	721	CAGCATACAGGGAGCAGACATCCTGSCCGGTGAGCCACCCGCTGGTCAGGGGCTG 780
DB	721	
QY	781	CTGGACCAGTTTGAGACCCGCAAGACCTCATCTCTCATCTCTGAGAGCTGTGCTCATCCGAG 840
DB	781	
QY	841	GAGCTGTGGACCGCCTGTACAGGAAGGCGTGTGACGGAGCCGAGGTCAGGTCAC 900
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QY	901	ATCCAGCAGCTGTTGGAAGGGGCTGCACCTACCTGTGACAGCCATGGCGTTCTCCACTGGAC 960
DB	901	
QY	961	ATAAGCCCTCTAACATCCTGATGGTGTATCTGCTGCCCGGGAAGACATTAANATCTGGAC 1020
DB	961	

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Db 2101 TCTCCGAGCACCCCGCCCTTCTCGAGGGCTCGGTGAGGCACAGCGACTGCCCTCA 2160
QY 2161 GCCCCTCCGGGGGGCCCTTATCAGGGACATGGGGCACCTCAGGGCTCCAAAGCAGCTT 2220
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Db 2281 TGGGGGACGACGCCCTTCTTCCACCCCAAGCAGGGTTCTGCCCCCAAGAGGGCTGC 2340
QY 2341 AGCCCCCAGCAGAGTGGCCCATGGCCCTCTGCTCTCTCTCCCTCCAGGATCTTGAAA 2400
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Db 2401 GAGGCCCTTATGATCCCTCAAGCCCTTCTTGGGACAGCCCAAGGACCCCTTGCCTT 2460
QY 2461 GCCAAGCAGCCCCCATGAGCTAAGATGGGCTTGAGACATCTCTCTCTCTGG 2520
Db 2461 GCCAAGCAGCCCCCATGAGCTAAGATGGGCTTGAGACATCTCTCTCTCTGG 2520
QY 2521 AGGCCAAACCCGGCCCTTGCAGTCTCCACAGGCTCAGCTCCACAGGAGCTCTTCCCAA 2580
Db 2521 AGGCCAAACCCGGCCCTTGCAGTCTCCACAGGCTCAGCTCCACAGGAGCTCTTCCCAA 2580
QY 2581 GTGAGCTCTCAGGCTGGCTCTCCAGTGGGCAAGAGCTGAGCTCTCTCTCTGGAT 2640
Db 2581 GTGAGCTCTCAGGCTGGCTCTCCAGTGGGCAAGAGCTGAGCTCTCTCTCTGGAT 2640
QY 2641 GCGAGGGCTGACCCAGAGGCTGAGGATCTGTCCGACTCCACACCCACTTTCAGCGG 2700
Db 2641 GCGAGGGCTGACCCAGAGGCTGAGGATCTGTCCGACTCCACACCCACTTTCAGCGG 2700
QY 2701 CTTCAAGACAGTGACCATGCGAAGTCTCTCTGGTGTGCGGGGCTAGCAGGC 2760
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QY 3181 GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCTCCCTAGGAGGAGCTGGCCGAG 3240

Db 3181 GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCTCCCTAGGAGGAGCTGGCCGAG 3240
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QY 258 CCGAGGCCCCATCCATCAGAGTAAACATCGAGGATGTGCAGGACACAGAGGCGGAAC 317
Db 3116 CGCACGCCCCCATCCATCCATGAGGTAAACATCGAGGATGTGCAGGACACAGAGGCGGAAC 3175
QY 318 GGGCCCAATTGAGGCTATCATTTAGGGGCGACCCACAGCCCTCGGTGACCTGGTCAAGGA 377
Db 3176 GGGCCCAATTGAGGCTATCATTTAGGGGCGACCCACAGCCCTCGGTGACCTGGTCAAGGA 3235
QY 378 CAGCGTCCAGCTGGTGACAGCACCGGGCTTAGCCAGCAGCAGGAAGGACACACATATCTC 437
Db 3236 CAGCGTCCAGCTGGTGACAGCACCGGGCTTAGCCAGCAGCAGGAAGGACACACATATCTC 3295
QY 438 CTTGGTCTGAGCAGTGGCTCGAGAGTGCAGGAGTGCAGTCTTATAGAGTCAAGAGGA 617
Db 3296 CTTGGTCTGAGCAGTGGCTCGAGAGTGCAGGAGTGCAGTCTTATAGAGTCAAGAGGA 3355
QY 498 CACTGGTGGCAGGTCTCTGCAAGCAGAGCTGTGTGTGTGGGGGGGCAATAGAGCC 557
Db 3356 CACTGGTGGCAGGTCTCTGCAAGCAGAGCTGTGTGTGTGGGGGGGCAATAGAGCC 3415
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Db 3416 GGAATCAGAGAGCAAGAGCCAGCGAGGAGTGCAGTCTTATAGAGTCAAGAGGA 3475
QY 618 GATTGGAGGGGGTGTGTGGCTTCGTAAGAGTGCAGCAGCAAGAGGAACAAGATCTT 677
Db 3476 GATTGGAGGGGGTGTGTGGCTTCGTAAGAGTGCAGCAGCAAGAGGAACAAGATCTT 3535
QY 678 GTGGCTGCCAAGTTTCATCCCTCAGGAGCAGAACTCGGGGCCAGGCATACAGGGAGCG 737
Db 3536 GTGGCTGCCAAGTTTCATCCCTCAGGAGCAGAACTCGGGGCCAGGCATACAGGGAGCG 3595
QY 738 AGACATCTCGGCGCTGAGCCACCGCTGTGTGACGGGGCTGTGGACCAAGTTTGAGAC 797
Db 3596 AGACATCTCGGCGCTGAGCCACCGCTGTGTGACGGGGCTGTGGACCAAGTTTGAGAC 3655
QY 798 CCGCAGAGACCTCATCTCATCTGAGCTGTGCTCATCCGAGGAGCTGTGAGCCGCT 857
Db 3656 CCGCAGAGACCTCATCTCATCTGAGCTGTGCTCATCCGAGGAGCTGTGAGCCGCT 3715
QY 858 GTACAGAGGGGGTGTGACGAGGCGCAGGTCAAGTCTACATCAGAGCTGTGGA 917
Db 3716 GTACAGAGGGGGTGTGACGAGGCGCAGGTCAAGTCTACATCAGAGCTGTGGA 3775
QY 918 GGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAGAGCCCTCTAACAT 977
Db 3776 GGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAGAGCCCTCTAACAT 3835
QY 978 CCTGATGTGCTATCTGCGGGGAGACATTAATCTTGGACTTTGGCTTTGCCAGAA 1037
Db 3836 CCTGATGTGCTATCTGCGGGGAGACATTAATCTTGGACTTTGGCTTTGCCAGAA 3895
QY 1038 CATCACCCAGCAGAGCTCAGTTAGCCAGTACGGCTCCCTGAGTTCTGCTCCCGCGA 1097
Db 3896 CATCACCCAGCAGAGCTCAGTTAGCCAGTACGGCTCCCTGAGTTCTGCTCCCGCGA 3955
QY 1098 GATCATCCAGCAGAACCTGTGAGCGAGAGCTCCGACATTTGGGCGCATGGGTGTATCTC 1157
Db 3956 GATCATCCAGCAGAACCTGTGAGCGAGAGCTCCGACATTTGGGCGCATGGGTGTATCTC 4015
QY 1158 CTACCTCAGCTGACTGTCTCATPCCCATTTGCGCGGAGAGTGAACGTGCCACCCCTCT 1217
Db 4016 CTACCTCAGCTGACTGTCTCATPCCCATTTGCGCGGAGAGTGAACGTGCCACCCCTCT 4075
QY 1218 GAACGTCTTGGAGGGGCGGTGTATGAGAGAGCCCATGCTGCGCACTCAGCGAAGA 1277
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QY 1278 CGCCAAAGACTTTCATCAAGGCTACGTTGAGAGAGCCCTCAGGGCGGGCTTAGTGGCG 1337
Db 4136 CGCCAAAGACTTTCATCAAGGCTACGTTGAGAGAGCCCTCAGGGCGGGCTTAGTGGCG 4195

QY 1338 CCAGTGCCTCTCCCAACCCCTGTTCTCTGAAATCAATGCTGCGGAGGAGGCCACCTTCAT 1397
Db 4196 CCAGTGCCTCTCCCAACCCCTGTTCTCTGAAATCAATGCTGCGGAGGAGGCCACCTTCAT 4255
QY 1398 GAACAGCAAGCAGCTCAAGTTCTCTGCGCGCAGAGTCCGCTGCGAGCTTCCTGATGAG 1457
Db 4256 GAACAGCAAGCAGCTCAAGTTCTCTGCGCGCAGAGTCCGCTGCGAGCTTCCTGATGAG 4315
QY 1458 CTCAAGTCCATCTCTGTTGATGCTCCTCATCTCTGAGCTGCTGCGGGGCGCCACCGACAG 1517
Db 4316 CTCAAGTCCATCTCTGTTGATGCTCCTCATCTCTGAGCTGCTGCGGGGCGCCACCGACAG 4375
QY 1518 CCGCTCCCTCGGCGTAGCCCGGACCTCTCAGAGGACACTGCTGCTCAGATTCCTCAGATTCCTC 1577
Db 4376 CCGCTCCCTCGGCGTAGCCCGGACCTCTGAGAGGACACTGCTGCTCAGATTCCTCAGATTCCTC 4435
QY 1578 TCTCTCTCTGACAAACAGAGCTGCGCCCAATTTGCGGGCTTAAGTCACTGCAACCTCCCTC 1637
Db 4436 TCTCTCTCTGACAAACAGAGCTGCGCCCAATTTGCGGGCTTAAGTCACTGCAACCTCCCTC 4495
QY 1638 GGTGACACACTCACTGCTGACACCCCGGGGCTTCTGCGGCGCTCCGCGAGAGCTGCG 1697
Db 4496 GGTGACACACTCACTGCTGACACCCCGGGGCTTCTGCGGCGCTCCGCGAGAGCTGCG 4555
QY 1698 TGAGAAAGCCGAGGCTGAGGCTCCACGAGAGCCCGAGCTCCGCTGCTCATCTCCCGA 1757
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QY 1818 GTTCTACACACAGCGGCTGAGAGCTCCAGAGCGGCTGAGAGCGGCTCCGCGGAGAGAGCG 1877
Db 4676 GTTCTACACACAGCGGCTGAGAGCTCCAGAGCGGCTGAGAGCGGCTCCGCGGAGAGAGCG 4735
QY 1878 GCACCCGCGCGCGGCGGACCTGTCTGAAGGGCGGCTCATTTGCGGGGCGCTGCGAG 1937
Db 4736 GCACCCGCGCGCGGCGGACCTGTCTGAAGGGCGGCTCATTTGCGGGGCGCTGCGAG 4795
QY 1938 CCTGGCGAGGACCTGATGAGACCGCTGCTGAGAGGAGGCGCGCCAGAGGAGGAGCA 1997
Db 4796 CCTGGCGAGGACCTGATGAGACCGCTGCTGAGAGGAGGCGCGCCAGAGGAGGAGCA 4855
QY 1998 GGCCACCTCTGCGCCAAAGCCCTCATTTGAGAGCTGCGCTCCGCTGCTGCTGCTG 2057
Db 4856 GGCCACCTCTGCGCCAAAGCCCTCATTTGAGAGCTGCGCTCCGCTGCTGCTGCTG 4915
QY 2058 CACCCACTTGGCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCAGCCCGG 2117
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QY 2298 TTTCTGCGCACCCCAAGCAGGGTTCTGCGCCCGCAGAGAGGCTGCGAGCCCGCAGCAGT 2357
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QY 2358 TGCCCGCATGCGCTCTGCTCTCTCTCAGAGTCTTCAAGAGAGGCGCCCTTAGTACC 2417
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3798 GTACACTCTGAGCTGAGCAATGCGCTGGGACAGTACACCAACGGCGTCTCCGGAA 3857

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6836 CCTAGAGGGCGAGCTGGACACACATGGCCCTTCGCACATCTTTGACTGCTGTACTGTAC 6895

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6896 CAGCAAGCTTCTCCGGGGTGGCACTTACACTTTCGCAACGGCATGTGTACGAAGCGAGG 6955

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6956 AATGGGTCCCTACAGCAGGCCCTTCGGAGCAAGTCTCTCTGGAGGGGCCACAGCACCTGGC 7015

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7196 CTCTGGCGAATACGAGCCCTCAAGGGCTTGGCCACCGCATCTGGCCAGCTGCACGC 7255

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7256 AGCTTACTCAGCCCCCGCACCTGGTGCTCATCTTGGAGTGTGTCTCTGGGCCGAGCT 7315

4458 GCTCCCTGCTGGCCAGAGGCGCTCTTACTCAGATCTTGAGGTGAAGACCTTACCTGTG 4517

7316 GCTCCCTGCTGGCCAGAGGCGCTCTTACTCAGATCTTGAGGTGAAGACCTTACCTGTG 7375

4518 GCAGATTTGAGTGGCAACCCAGTACCTGCACAAACAGACATCTCTGCACCTGCACCTGAG 4577

7376 GCAGATTTGAGTGGCAACCCAGTACCTGCACAAACAGACATCTCTGCACCTGCACCTGAG 7435

4578 GTCCGAGAAATGATCATCACCGGAATAAACTGTCTCAAGTCTGTGACCTGGGCAATGC 4637

7436 GTCCGAGAAATGATCATCACCGGAATAAACTGTCTCAAGTCTGTGACCTGGGCAATGC 7495

QY 4638 ACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAAGGACTACTAGAGAC 4697
Dd 7496 ACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAAGTTCAAGGACTACTAGAGAC 7555
QY 4698 CATGCTCCAGAGCTCTGAGGCGCCAGGAGGCTGTTCCACAGACAGACATCTGGGCCAT 4757
Dd 7556 CATGCTCCAGAGCTCTGAGGCGCCAGGAGGCTGTTCCACAGACAGACATCTGGGCCAT 7615
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Dd 7616 CGGTGTGACAGCTTCATCATCTGTCAGCGCCAGTAGTACCCCGGTGAGCAGCGAGGGTGCACG 7675
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Dd 7736 GTCCGGGGCGCCCGTCCCTTCTGCGCAGCACTCTGTGCGCCAGCCCTGGGGCGCGCC 7795
QY 4938 CTGGCGCTCCAGCTGCTGAGTGCCTGCTGCTGCTAAACAGAGAGGGCGCCGCTGCTGCGG 4997
Dd 7796 CTGGCGCTCCAGCTGCTGAGTGCCTGCTGCTGCTAAACAGAGAGGGCGCCGCTGCTGCGG 7855
QY 4998 GCCCGCGCCGCTGACCTTCCCTACCGCGCGCTGCGCTGCTGCTGCGCAATCGCGAGAA 5057
Dd 7856 GCCCGCGCCGCTGACCTTCCCTACCGCGCGCTGCGCTGCTGCTGCGCAATCGCGAGAA 7915
QY 5058 GAGAGCGCGCTGCTGACAGAGGCGACACCTGCGCCAGGTCGCTGAGGTCCCGCG 5117
Dd 7916 GAGAGCGCGCTGCTGACAGAGGCGACACCTGCGCCAGGTCGCTGAGGTCCCGCG 7975
QY 5118 GCCACACCTTGGTCTCCCGCTGGGGTCTGCTGCGAGCGCGCCCAATAAAAAACGACAGC 5177
Dd 7976 GCCACACCTTGGTCTCCCGCTGGGGTCTGCTGCGAGCGCGCCCAATAAAAAACGCGCAG 8035
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Dd 8036 CGGCGGAGAAAAAATAAAAAAATAAAAAA 8065
RESULT 5
ID ABX11642
XX ABX11642 standard; cDNA: 24120 BP.
XX AC ABX11642;
XX DT 09-MAY-2003 (first entry)
XX DE Human serine/threonine or protein kinase 12599, cDNA.
XX KW Human; ss: gene; serine/threonine kinase; protein kinase; 12599;
KW cardiovascular disease; heart failure; myocardial infarction;
KW blood vessel disorder; atherosclerosis; Kaposi's sarcoma;
KW blood platelet disorder; thrombocytopaenia; leukaemia; Hodgkin's disease;
KW haemolytic anaemia; cellular proliferative disorder; cancer;
KW protein kinase disorder; autoimmune disorder; diabetes mellitus;
KW psoriasis; inflammatory bowel disease; rheumatoid arthritis;
KW multiple sclerosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT 5'UTR 1..71
FT CDS /*tag= a
FT 72..23978
FT /*tag= b
FT /*product= "Kinase 12599"
FT /*note= "This CDS is specifically claimed in claim 2"
FT 3'UTR 23979..24120
FT /*tag= c
XX

US2002168742-A1.
14-NOV-2002.
15-FEB-2002; 2002US-00077130.
15-FEB-2001; 2001US-0269201P.
(MILL-) MILLENNIUM PHARM INC.
Kapeller-Libermann R, Acton SL;
WPI: 2003-298729/29.
P-PSDB; ABG76187.
Novel isolated human protein kinase, designated 59079 or 12599 polypeptide, useful as diagnostic and therapeutic agents for preventing cardiovascular diseases, proliferative disorders, and protein kinase disorders.
Claim 2; Page 58-84; 119pp; English.
The invention relates to an isolated human serine/threonine or protein kinase, 59079 or 12599 polypeptide, encoded by nucleic acid molecule comprising at least 85% identity to the nucleic acids appearing as ABX11641 and ABX11642 or their complement, a naturally occurring variant of the kinases or their fragments. Also included are a non-human host cell containing the nucleic acids, an antibody specific for the proteins, identifying a compound which binds to the kinase (by contacting the kinase or a cell expressing the kinase with a test compound and determining whether the kinase binds to the test compound) and modulating the activity of kinase using the identified compound. The kinases and their encoding nucleic acids are useful as diagnostic and therapeutic agents for preventing a disease or condition associated with an aberrant or unwanted 59079 or 12599 activity in a subject, including cardiovascular diseases such as heart failure, and myocardial infarction; disorders involving blood vessels such as atherosclerosis, and Kaposi's sarcoma; blood platelets disorder such as thrombocytopaenia, leukaemia, Hodgkin's disease, haemolytic anaemia; cellular proliferative disorders such as cancer; and protein kinase disorders such as autoimmune diseases, rheumatoid arthritis, and multiple sclerosis (many examples of diseases and disorders are included in the specification). The kinases, their encoding nucleic acids and antibodies are useful in screening assays, diagnostic assays, prognostic assays, and monitoring clinical trials and pharmacogenomics). The kinases and their encoding nucleic acids are useful as query sequences to perform a search against public databases to identify other family members or related sequences. The present sequence encodes the kinase 12599
Sequence 24120 BP; 4719 A; 7265 C; 8278 G; 3858 T; 0 U; 0 Other;
Query Match 94.9%; Score 4940.4; DB 7; Length 24120;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4944; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 258 CCCAGGCCCCCATCCATGCAAGTAAACCATGAGATGTGAGGACAGAGCGGGAAC 317
Dd 19130 CGACGCGCCCCCATCCATGCAAGTAAACCATGAGATGTGAGGACAGAGCGGGAAC 19189
QY 318 GGCCCAATTCGAGGCTATCATTTAGGCGGACCCACAGCCCTCGGTGACTGTACAGGA 377
Dd 19190 GGCCCAATTCGAGGCTATCATTTAGGCGGACCCACAGCCCTCGGTGACTGTACAGGA 19249
QY 378 CAGCGTCCAGTGTGTGACAGACCCCGGCTTAGCCAGCAGCAAGGACCAACATCTC 437
Dd 19250 CAGCGTCCAGTGTGTGACAGACCCCGGCTTAGCCAGCAGCAAGGACCAACATCTC 19309
QY 438 CTTGGTGTGAGGCATGTGGCTCGAAGGATGCGCGCTTTACACCTGCGCTGGCCCAAAA 497
Dd 19310 CTTGGTGTGAGGCATGTGGCTCGAAGGATGCGCGCTTTACACCTGCGCTGGCCCAAAA 19369

QY	498	CACTGGTGGCCAGGTGCTCTGCAAGGCAGACAGCTGCTGGTCTTGCGGGGGGACAATAGACC	557
DB	19370	CACTGGTGGCCAGGTGCTCTGCAAGGCAGACAGCTGCTGGTCTTGCGGGGGGACAATAGACC	19429
QY	558	GGACTCAGAGAAAGCAAAAGCCACCGGAGGAGAGTGCACCTCTTATAGAGTCAAGAGGGA	617
DB	19430	GGACTCAGAGAAAGCAAAAGCCACCGGAGGAGAGTGCACCTCTTATAGAGTCAAGAGGGA	19489
QY	618	GATTGGAAAGGGCGTGTGGCTTCGTAAAAGAGTGCAGACAAAGAGAAACAAGATCTT	677
DB	19490	GATTGGAAAGGGCGTGTGGCTTCGTAAAAGAGTGCAGACAAAGAGAAACAAGATCTT	19549
QY	678	GTGGCGTGGCAAGTTTCATCCCTACGGAGCAGAACTCGGGCCACGGCATACAGGAGCG	737
DB	19550	GTGGCGTGGCAAGTTTCATCCCTACGGAGCAGAACTCGGGCCACGGCATACAGGAGCG	19609
QY	738	AGACATCTCGGCGGCTGAGCCACCGCTGTGTACGGGGGTGCTGGACCAAGTTTGAGAC	797
DB	19610	AGACATCTCGGCGGCTGAGCCACCGCTGTGTACGGGGGTGCTGGACCAAGTTTGAGAC	19669
QY	798	CCGCAAGACCCCTCATCTTCATCCTCGAGCTGTGCTCATCCGAGGAGTGCTGGACCGCT	857
DB	19670	CCGCAAGACCCCTCATCTTCATCCTCGAGCTGTGCTCATCCGAGGAGTGCTGGACCGCT	19729
QY	858	GTACAGGAAGGGCGTGGTGAACGGAGCCGAGGTCAAGTCTACATCCAGCAGCTGTGTGA	917
DB	19730	GTACAGGAAGGGCGTGGTGAACGGAGCCGAGGTCAAGTCTACATCCAGCAGCTGTGTGA	19789
QY	918	GGGGTGCACCTACCTGCAAGCATGTGGGTCTCCACCTGGACATAAAGCCCTCTAACAT	977
DB	19790	GGGGTGCACCTACCTGCAAGCATGTGGGTCTCCACCTGGACATAAAGCCCTCTAACAT	19849
QY	978	CTGTATGTGTGATCTCTGCCGGGAGACATTAATATCTGCACATTTGGCTTTGCCAGAA	1037
DB	19850	CTGTATGTGTGATCTCTGCCGGGAGACATTAATATCTGCACATTTGGCTTTGCCAGAA	19909
QY	1038	CATCATCCCGCAGCAGAGCTGCATTTGAGCCAGTACGGCTCCCTGAGTTGCTCTCCCGGA	1097
DB	19910	CATCATCCCGCAGCAGAGCTGCATTTGAGCCAGTACGGCTCCCTGAGTTGCTCTCCCGGA	19969
QY	1098	GATCATCCAGCAGAAACCTGTGAGCGAAAGCCCTCCGACATTTGGGCCCATGGGTGCATCTC	1157
DB	19970	GATCATCCAGCAGAAACCTGTGAGCGAAAGCCCTCCGACATTTGGGCCCATGGGTGCATCTC	20029
QY	1158	CTACCTCAGCGCTGACCTGCTCATCCCATTTGCGGGCGAGAGTGACGTCGACCGCTCT	1217
DB	20030	CTACCTCAGCGCTGACCTGCTCATCCCATTTGCGGGCGAGAGTGACGTCGACCGCTCT	20089
QY	1218	GAACTCTGGAGGGCGGTGTATGAGCAGAGCCCATGGCTGCCACCTCAGCGAAGA	1277
DB	20090	GAACTCTGGAGGGCGGTGTATGAGCAGAGCCCATGGCTGCCACCTCAGCGAAGA	20149
QY	1278	CGCCAAAGACTTCATCAAGCTACGCTCCAGAGAGCCCTCAGGCGCGGCTAGTCGGCG	1337
DB	20150	CGCCAAAGACTTCATCAAGCTACGCTCCAGAGAGCCCTCAGGCGCGGCTAGTCGGCG	20209
QY	1338	CGAGTGCCTCTCCGACCGCTGGTTCTGAAATCCATGCTCGGAGAGGGGCCACTTCAT	1397
DB	20210	CGAGTGCCTCTCCGACCGCTGGTTCTGAAATCCATGCTCGGAGAGGGGCCACTTCAT	20269
QY	1398	CAACACCAAGCAGCTCAAGTTCTCTCGCCCGGCAAGTCGCTGGCAGAGGTTCCCTGTAGAG	1457
DB	20270	CAACACCAAGCAGCTCAAGTTCTCTCGCCCGGCAAGTCGCTGGCAGAGGTTCCCTGTAGAG	20329
QY	1458	CTCAAGTCCCATCTGGTGTGCGCTCCATCCCTGAGCTGCTGGGGGCCACACCGGACAG	1517
DB	20330	CTCAAGTCCCATCTGGTGTGCGCTCCATCCCTGAGCTGCTGGGGGCCACACCGGACAG	20389
QY	1518	CCCCCTCCTCGCGTAGCCGGCAGCTCTGAGGGAGACCTGGTGGCTCTCCAGTTCTCTC	1577
DB	20390	CCCCCTCCTCGCGTAGCCGGCAGCTCTGAGGGAGACCTGGTGGCTCTCCAGTTCTCTC	20449
QY	1578	CTCCTCCTCTGACAAACGAGCTCGCCCCATTTGCCGGGCTAAAGTCACTGCCACCGCTCCCC	1637

20450	CTTCTTCCTCTGACAAACGAGCTTCGCCCATTTTCCCGGGCTAAGTCACTTCGCACACCTCCCC	Db
1638	GGTGAACAACATCAACATTCGTGACACCCCGGGGCTTCTTGGGCCCTTCGGCCACGCTTGCC	Qy
20510	GGTGAACAACATCAACATTCGTGACACCCCGGGGCTTCTTGGGCCCTTCGGCCACGCTTGCC	Db
1698	TGAGAAAGCCGAGGCGAGTGAAGCGCTCCACCGAGGCCCCAGCTCCGCTGCGCATCTCCCGA	Qy
20570	TGAGAAAGCCGAGGCGAGTGAAGCGCTCCACCGAGGCCCCAGCTCCGCTGCGCATCTCCCGA	Db
1758	GGGTGCGGGGCGACCGGCCGCCAGAGCTGGTGCCTCCCGGCACAGAGCTCATTCGCGACCT	Qy
20630	GGGTGCGGGGCGACCGGCCGCCAGAGCTGGTGCCTCCCGGCACAGAGCTCATTCGCGACCT	Db
1818	GTCTTACCAACAGGCGGGTGAGACCCCTTGAGCACGGGGCCCTTGCCCCGGGAGCAGGCG	Qy
20690	GTCTTACCAACAGGCGGGTGAGACCCCTTGAGCACGGGGCCCTTGCCCCGGGAGCAGGCG	Db
1878	GCACCCCGGCCCGGGCGGCACCTGCTGAAGGGCGGCTACATTCGCGGGCGCTGTCACGG	Qy
20750	GCACCCCGGCCCGGGCGGCACCTGCTGAAGGGCGGCTACATTCGCGGGCGCTGTCACGG	Db
1938	CTTGCGCAGGCACATGATGAGACACCGCGTGTGTGAGGAGGAGGCCGCCAGGAGAGACA	Qy
20810	CTTGCGCAGGCACATGATGAGACACCGCGTGTGTGAGGAGGAGGCCGCCAGGAGAGACA	Db
1998	GGCCACCCCTCTTGGCCAAAGCCCCCTCATTCGAGACTGCCCCCTCGGCTGCTGCTCTGG	Qy
20870	GGCCACCCCTCTTGGCCAAAGCCCCCTCATTCGAGACTGCCCCCTCGGCTGCTGCTCTGG	Db
2058	CACCCACATTGGCCACAGCACTCCCTCGGAACATGACTCTCCGAGCACCCCCCG	Qy
20930	CACCCACATTGGCCACAGCACTCCCTCGGAACATGACTCTCCGAGCACCCCCCG	Db
2118	CCCTTCTCGAGGCGTGGGTGAGGACAGCAGCATGCTTTCAGCCCTTCGGGGGGGC	Qy
20990	CCCTTCTCGAGGCGTGGGTGAGGACAGCAGCATGCTTTCAGCCCTTCGGGGGGGC	Db
2178	CCCTATCAGGACATGGGGCACCCCTCAGGGGTCCAAAGCAGCTTCATCCACTGGTGCCCA	Qy
21050	CCCTATCAGGACATGGGGCACCCCTCAGGGGTCCAAAGCAGCTTCATCCACTGGTGCCCA	Db
2238	CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCTTTGGGGGAGCCAGCCCC	Qy
21110	CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCTTTGGGGGAGCCAGCCCC	Db
2298	TTTCTGCCACCCCAAGCAGAGGTTCTGCCCCCGCAGGAGGGTGCAGCCCCACCCAGGAGT	Qy
21170	TTTCTGCCACCCCAAGCAGAGGTTCTGCCCCCGCAGGAGGGTGCAGCCCCACCCAGGAGT	Db
2358	TGCCCCATGCCCTCCTTGGCTCCTTCCCTCCAGGATCTTGCAAGAGAGGCCCCCTTAGTACC	Qy
21230	TGCCCCATGCCCTCCTTGGCTCCTTCCCTCCAGGATCTTGCAAGAGAGGCCCCCTTAGTACC	Db
2418	CTCAAGCCCTCTTCTGGGACAGCCCGCAGGACACCCCTTGCCCTTCGCACAGAGCCGCC	Qy
21290	CTCAAGCCCTCTTCTGGGACAGCCCGCAGGACACCCCTTGCCCTTCGCACAGAGCCGCC	Db
2478	ATTGACTCTAAGATGGGGCTGGAGACATCTCTTCTTCTGGGAGGCCAAAAACCGGCC	Qy
21350	ATTGACTCTAAGATGGGGCTGGAGACATCTCTTCTTCTGGGAGGCCAAAAACCGGCC	Db
2538	CTGCAGTTCCCAAGGTCAGCTCCACAGGCGAGCTCTTCCCAAGTGAAGTCCCTCAGGCT	Qy
21410	CTGCAGTTCCCAAGGTCAGCTCCACAGGCGAGCTCTTCCCAAGTGAAGTCCCTCAGGCT	Db
2598	GGGCTCTCCAGGTGGGCACAGAGCTTGCCCTCCTCGATGTCGGAGGGCTTGGACCA	Qy
21470	GGGCTCTCCAGGTGGGCACAGAGCTTGCCCTCCTCGATGTCGGAGGGCTTGGACCA	Db
2658	GGAGGCTGAGGATCTGTCCGACTCCACACCACTTTCAGCGCGCTCAGGAAAGGTTGAC	Qy

Db	21530	GGAGGCTGAGGATCTGTTCGACTCCACACCCACTTTCAGCGGCGCTTCAGGAACAGGCGAC	21581
Qy	2718	CATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGACGGCGTGGTGGCTATGGCAC	2777
Db	21590	CATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGACGGCGTGGTGGCTATGGCAC	21649
Qy	2778	CTTTGGCTTTGGTGAGATGCAGGGGGCATGCTGGGCGAGGGGCCCATGTGGGCGACGAT	2837
Db	21650	CTTTGGCTTTGGTGAGATGCAGGGGGCATGCTGGGCGAGGGGCCCATGTGGGCGCAGGAT	21709
Qy	2838	AGCCTGGGCTGTGTCCTCAGTTCGAGGAGGAGCAGGAGGAGGCCAGGGCTGATGCCCA	2897
Db	21710	AGCCTGGGCTGTGTCCTCAGTTCGAGGAGGAGCAGGAGGAGGCCAGGGCTGATGCCCA	21769
Qy	2898	GTGCGAGGAGCAGCAGAGGCCAGGGCTCAGAGCCCACTGCCGCCCAAGCTCAGTGCAGAGCC	2957
Db	21770	GTGCGAGGAGCAGCAGAGGCCAGGGCTCAGAGCCCACTGCCGCCCAAGCTCAGTGCAGAGCC	21829
Qy	2958	TGTGCTGTAGGTCGGCAGGGCTCCCAACCAAGGAGCTCTCCAGAGCCCAACCCATGGAGGA	3017
Db	21830	TGTGCTGTAGGTCGGCAGGGCTCCCAACCAAGGAGCTCTCCAGAGCCCAACCCATGGAGGA	21889
Qy	3018	CATCGGCGAGGTCCTCCCTGGTCAGATCCGGACCTGTCCAGGTGATCGGAGGGCGGCCGA	3077
Db	21890	CATCGGCGAGGTCCTCCCTGGTCAGATCCGGACCTGTCCAGGTGATCGGAGGGCGGCCGA	21949
Qy	3078	CACAATATCCTGTGAATTTTCGAGGTGAGCCCGGCTACCTCAACCTCTCAGACCTGTGA	3137
Db	21950	CACAATATCCTGTGGAATTTTCGAGGTGAGCCCGGCTACCTCAACCTCTCAGACCTGTGA	22009
Qy	3138	CGATATCAAGTACTCTCCCAATTCGAGTTTATGATCTTCAGGAAGTCCCCAAAGTCGGCTCA	3197
Db	22010	CGATATCAAGTACTCTCCCAATTCGAGTTTATGATCTTCAGGAAGTCCCCAAAGTCGGCTCA	22069
Qy	3198	GCCAGAGCGCCTCTCCCCCATGGCTGAGAGAGAGCTGGCCGAGTTTCCCGAGGCCCACTGTG	3257
Db	22070	GCCAGAGCGCCTCTCCCCCATGGCTGAGAGAGAGCTGGCCGAGTTTCCCGAGGCCCACTGTG	22129
Qy	3258	GCCTCGGCGAGGTGAACCTGGGCGCCCAACGACGGCTGGAGATCAACAGAGGAGTCAGAGGA	3317
Db	22130	GCCTCGGCGAGGTGAACCTGGGCGCCCAACGACGGCTGGAGATCAACAGAGGAGTCAGAGGA	22189
Qy	3318	TGTGGAGCGCTCTCTGGCAGAGGCTGCCGTGGGCGAGGAAGCGCAAGTGGTCTCTGCCGCTC	3377
Db	22190	TGTGGAGCGCGCTCTCTGGCAGAGGCTGCCGTGGGCGAGGAAGCGCAAGTGGTCTCTGCCGCTC	22249
Qy	3378	ACGCAGCCTCTTCCATTTCCCTGGGAGGCACCTGCCGCTGGATGATGAGCTGCAGAGCTGGG	3437
Db	22250	ACGCAGCCTCTTCCATTTCCCTGGGAGGCACCTGCCGCTGGATGATGAGCTGCAGAGCTGGG	22309
Qy	3438	GCTGCGTGAGAGAGTGAAGGCTCCGTGGAGACATCTCCGGATCTCTGAGGCGCAGGCC	3497
Db	22310	GCTGCGTGAGAGAGTGAAGGCTCCGTGGAGACATCTCCGGATCTCTGAGGCGCAGGCC	22369
Qy	3498	GGAAAGTCTGGAAGAGGAGGGGCCCCCAAGGAAGCCAGGCGCTTGCTTCTTCCCGGCT	3557
Db	22370	GGAAAGTCTGGAAGAGGAGGGGCCCCCAAGGAAGCCAGGCGCTTGCTTCTTCCCGGCT	22429
Qy	3558	CTCAGGCTCTGAGAGCTGGACCGGAGCGCCGACATTTCTTAGGGAGCTCTCAGATGAGAC	3617
Db	22430	CTCAGGCTCTGAGAGCTGGACCGGAGCGCCGACATTTCTTAGGGAGCTCTCAGATGAGAC	22489
Qy	3618	TGTGFTCTGGGCCAGTCAGTGACACTGGCTGCCAGTGTTCAGCCACGACGCTGCCCA	3677
Db	22490	TGTGFTCTGGGCCAGTCAGTGACACTGGCTGCCAGTGTTCAGCCACGACGCTGCCCA	22549
Qy	3678	GGCCACTGGAGCAAGACGGAGCCCCCTTGAGAGCAGACCGGTGTCATCTCTGC	3737
Db	22550	GGCCACTGGAGCAAGACGGAGCCCCCTTGAGAGCAGACCGGTGTCATCTCTGC	22609
Qy	3738	CACCTTCAAGACTTCCAGCTTCTCAACCATCTGTTGTTGGCTCAGGACCTGGGTGT	3797
Db	22610	CACCTTCAAGACTTCCAGCTTCTCAACCATCTGTTGTTGGCTCAGGACCTGGGTGT	22669

QY	3798	GTACACTGTGAGCGTGTGAGCAATGCGCTGGGGACAGTGTACCAACACGCGCGTCTCTCCGGAA	3857
DB	22670	GTACACTGTGAGCGTGTGAGCAATGCGCTGGGGACAGTGTACCAACACGCGCGTCTCTCCGGAA	22729
QY	3858	GGCAGAGCGCCCTCATCTTCGCCATCGCCCGATATCGGGGAGGTGTACCGGATGGGGT	3917
DB	22730	GGCAGAGCGCCCTCATCTTCGCCATCGCCCGATATCGGGGAGGTGTACCGGATGGGGT	22789
QY	3916	GCTGCTGGTGTGAGAGCGCGTGGAACTCTACGGCCCTGTGACCTACATTTGTGCAGTGCAG	3977
DB	22790	GCTGCTGGTGTGAGAGCGCGTGGAACTCTACGGCCCTGTGACCTACATTTGTGCAGTGCAG	22849
QY	3978	CCTAGAGGGGGGAGGTGTGACCAACTGTGCCCTTCGACATCTTTTGAATGTGTGTACTCTGCAC	4037
DB	22850	CCTAGAGGGGGGAGGTGTGACCAACTGTGCCCTTCGACATCTTTTGAATGTGTGTACTCTGCAC	22909
QY	4038	CAGCAAGCTCTCCCGGGGTGGCACCTTACACCTTCGCGACGCGCATGTGTCAAGAGCGAGG	4097
DB	22910	CAGCAAGCTCTCCCGGGGTGGCACCTTACACCTTCGCGACGCGCATGTGTCAAGAGCGAGG	22969
QY	4098	AATGGGTCCCTACAGACAGCCCTCGGAGCAAGTCTCTCTGGGAGGGCCGCCACCTGGC	4157
DB	22970	AATGGGTCCCTACAGACAGCCCTCGGAGCAAGTCTCTCTGGGAGGGCCGCCACCTGGC	23029
QY	4158	CTCTGAGGAGGAGCCAGGGCGGTGACCCAAACCCCTGCCAGCAAAAGACTTTCGC	4217
DB	23030	CTCTGAGGAGGAGCCAGGGCGGTGACCCAAACCCCTGCCAGCAAAAGACTTTCGC	23089
QY	4218	ATTCCAGACACAGATCCAGAGGGCGCTTACAGCTGTGTGGCAATGCTGGGAGAAGGC	4277
DB	23090	ATTCCAGACACAGATCCAGAGGGCGCTTACAGCTGTGTGGCAATGCTGGGAGAAGGC	23149
QY	4278	CAGCGGGCGGCGCTGGCGGCCAAGATCTATCCCTTACACCCCAAGACAGACAGCAGT	4337
DB	23150	CAGCGGGCGGCGCTGGCGGCCAAGATCTATCCCTTACACCCCAAGACAGACAGCAGT	23209
QY	4338	GCTGCGCGAATACGAGGCCCTCAAGGGGCGCTGCGCCACCCGACACCTTGGGCCACAGCTGCACGC	4397
DB	23210	GCTGCGCGAATACGAGGCCCTCAAGGGGCGCTGCGCCACCCGACACCTTGGGCCACAGCTGCACGC	23269
QY	4398	AGCCTACTTCAGCCCCCGCACCTTGTGCTCATCTTGGAGCTGTGCTCTGGGCCCGAGCT	4457
DB	23270	AGCCTACTTCAGCCCCCGCGACCTTGTGCTCATCTTGGAGCTGTGCTCTGGGCCCGAGCT	23329
QY	4458	GCTCCCTCGCTGGCGAGAGGGCTCTTACTCAGAACTCTGAGTGAAGGACTACTCTGTG	4517
DB	23330	GCTCCCTCGCTGGCGAGAGGGCTCTTACTCAGAACTCTGAGTGAAGGACTACTCTGTG	23389
QY	4518	GCAGATGTTGAGTGGCACCCAGTACTGTCAAAACAGACACATCTGTCACTTGGACCTTGAC	4577
DB	23390	GCAGATGTTGAGTGGCACCCAGTACTGTCAAAACAGACACATCTGTCACTTGGACCTTGAC	23449
QY	4578	GTCCGAGACATGATCATCACCGAATACAACTGCTCAAGTCTGTGACCTTGGGCCAATGC	4637
DB	23450	GTCCGAGACATGATCATCACCGAATACAACTGCTCAAGTCTGTGACCTTGGGCCAATGC	23509
QY	4638	ACAGAGCTTCAGCCAGGAGAAAGTGTCTGCCCTCAGACAAAGTTCAAGGACTACTTAGAGAC	4697
DB	23510	ACAGAGCTTCAGCCAGGAGAAAGTGTCTGCCCTCAGACAAAGTTCAAGGACTACTTAGAGAC	23569
QY	4698	CATGGCTCCAGAGCTCTCTGGAGGGCCAGGGGCGCTTTCACACAGACAGACATCTGGGCCAT	4757
DB	23570	CATGGCTCCAGAGCTCTCTGGAGGGCCAGGGGCGCTTTCACACAGACAGACATCTGGGCCAT	23629
QY	4758	CGGTGTGACAGCCTTTCATCTGCTGAGCGCCGAGTATCCCGTGTAGACGCGAGGGTGCACG	4817
DB	23630	CGGTGTGACAGCCTTTCATCTGCTGAGCGCCGAGTATCCCGTGTAGACGCGAGGGTGCACG	23689
QY	4818	CGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTCCGGCTGAGCCGCTGCTACTACGCGGGCT	4877
DB	23690	CGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTCCGGCTGAGCCGCTGCTACTACGCGGGCT	23749

Qy	1038	CATCACCCAGCAGAGCTGCAGTTTCAGCCAGTACGGCTCCCTCGAGTTTCGTCTCCCCCGGA	1097
Db	861	CATCACCCAGCAGAGCTGCAGTTTCAGCCAGTACGGCTCCCTCGAGTTTCGTCTCCCCCGGA	920
Qy	1098	GATCATCCAGAGAACCCCTGTGAGCGAAGCCTCGACATTTGGCGGCATGGGTGTCATCTC	1157
Db	921	GATCATCCAGAGAACCCCTGTGAGCGAAGCCTCGACATTTGGCGGCATGGGTGTCATCTC	980
Qy	1158	CTACCTCAGCCTGACCTTGCTCTCATGCCCATTTTGCGCGAGAGTGACCTGCCACCTCTCT	1217
Db	981	CTACCTCAGCCTGACCTTGCTCTCATGCCCATTTTGCGCGAGAGTGACCTGCCACCTCTCT	1040
Qy	1218	GAACTGCTTGGAGGGCGCGTGTTCATGGAGACGCCCATGGCTGCCACCTTCAGCGAAGA	1277
Db	1041	GAACTGCTTGGAGGGCGCGTGTTCATGGAGACGCCCATGGCTGCCACCTTCAGCGAAGA	1100
Qy	1278	CGCGAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCGCGGCTAGTGGCGC	1337
Db	1101	CGCGAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCGCGGCTAGTGGCGC	1160
Qy	1338	CCAGTGCTCTCCCAACCCCTGTTTCTCTGAAATCCATGCTCGCGAGGAGGCCACTTCAT	1397
Db	1161	CCAGTGCTCTCCCAACCCCTGTTTCTCTGAAATCCATGCTCGCGAGGAGGCCACTTCAT	1220
Qy	1398	CAACACCAAGCAGCTCAAGTTCCTCTGGCGCGAAGTGCCTGGAGCCTTCCTGTATGAG	1457
Db	1221	CAACACCAAGCAGCTCAAGTTCCTCTGGCGCGAAGTGCCTGGAGCCTTCCTGTATGAG	1280
Qy	1458	CTCAAGTCCATCTCTGTGTGATGGCTCCATCTCCTGAGCTGTCTCGGGGCCCAACCCGACAG	1517
Db	1281	CTCAAGTCCATCTCTGTGTGATGGCTCCATCTCCTGAGCTGTCTCGGGGCCCAACCCGACAG	1340
Qy	1518	CCCTCCCTCGGCTTACCCCGGACCTCTCTCAGGGACACTGTGTGCTCTCCAGTTCCTC	1577
Db	1341	CCCTCCCTCGGCTTACCCCGGACCTCTCTCAGGGACACTGTGTGCTCTCCAGTTCCTC	1400
Qy	1578	CTCTCTCTTGACAACGAGCTGCGCCCATTTGCGCGGCTTAAGTCACTGSCACCCCTCCCC	1637
Db	1401	CTCTCTCTTGACAACGAGCTGCGCCCATTTGCGCGGCTTAAGTCACTGSCACCCCTCCCC	1460
Qy	1638	GGTGACACACTCACCACTGCTGCACCCCGGGCTTCTGCGGCGCTCGGCGACGCTGCC	1697
Db	1461	GGTGACACACTCACCACTGCTGCACCCCGGGCTTCTGCGGCGCTCGGCGACGCTGCC	1520
Qy	1698	TGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCCCAGCTCCGCGCTGATCTCCCGGA	1757
Db	1521	TGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCCCAGCTCCGCGCTGATCTCCCGGA	1580
Qy	1758	GGGTGCGGGGCCACGGCGCCGAGGGCTGCGTGCCCGGCGACAGCGTCACTCCGACGCT	1817
Db	1581	GGGTGCGGGGCCACGGCGCCGAGGGCTGCGTGCCCGGCGACAGCGTCACTCCGACGCT	1640
Qy	1818	GTTCATCAACAGCGCGGTGAGAGCCCTGAGCACGGGGCCCTGGCCCGGGAGCAGGGG	1877
Db	1641	GTTCATCAACAGCGCGGTGAGAGCCCTGAGCACGGGGCCCTGGCCCGGGAGCAGGGG	1700
Qy	1878	GCACCCGCGCGGGCGGGCACCTGCTGAAGGGCGGCTACATTGCGGGGGCGTGCACAGG	1937
Db	1701	GCACCCGCGCGGGCGGGCACCTGCTGAAGGGCGGCTACATTGCGGGGGCGTGCACAGG	1760
Qy	1938	CCTGCGCAGACCACTGATGAGCAACCGCTGTCTGAGAGAGAGGCCCGCAGGGAGAGCA	1997
Db	1761	CCTGCGCAGACCACTGATGAGCAACCGCTGTCTGAGAGAGAGGCCCGCAGGGAGAGCA	1820
Qy	1998	GGCCACCTCTCTGGCCAAAGCCCTCATTTCCAGACTGCGCTTCGGGCTGCTGCTCTGG	2057
Db	1821	GGCCACCTCTCTGGCCAAAGCCCTCATTTCCAGACTGCGCTTCGGGCTGCTGCTCTGG	1880
Qy	2058	GACCCACTTGGCCCTCGGCACAGCACTCTCCTTGAAACATGACTCTCGAGACACCCCGCG	2117
Db	1881	GACCCACTTGGCCCTCGGCACAGCACTCTCCTTGAAACATGACTCTCGAGACACCCCGCG	1940
Qy	2118	CCCTCTCTCGAGAGCCCTGCGGTGAGGCACAGCGACTGCTTTCAAGCCCTCTCGGGGGGGC	2177

Db	1941	CCCCTCCTCGAGGCGCTGCGGTGAGGCGACAGCGAC	TGCCTTCACGCCCTCCGGGCGGC	2000
Qy	2178	CCCTATCAGGACATGGGCGACCCCTCAGGGCTCCAGCAGCTTC	CAATCCACTGGTGGCCA	2237
Db	2001	CCCTATCAGGACATGGGCGACCCCTCAGGGCTCCAGCAGCTTC	CAATCCACTGGTGGCCA	2060
Qy	2238	CCCAGGCACTGCTCAGCAGAGAGGCGCATCCCGGAGAGCCCT	TGGGGGAGCAGCAGCCCC	2297
Db	2061	CCCAGGCACTGCTCAGCAGAGAGGCGCATCCCGGAGAGCCCT	TGGGGGAGCAGCAGCCCC	2120
Qy	2298	TTTCTGCGACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC	AGCCCCCACCACCCAGCAGT	2357
Db	2121	TTTCTGCGACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC	AGCCCCCACCACCCAGCAGT	2180
Qy	2358	TGCCCATGCCCTCTGGCTCTCTCCCTCAGGATCTTGAAAGAGG	CCCCCTTAGTACC	2417
Db	2181	TGCCCATGCCCTCTGGCTCTCTCCCTCAGGATCTTGAAAGAGG	CCCCCTTAGTACC	2240
Qy	2418	CTCAAGCCCTTCTTGGGACAGCCCCCAGGCACCCCTGCCCC	TGCCAAAGCAAGCGCCCC	2477
Db	2241	CTCAAGCCCTTCTTGGGACAGCCCCCAGGCACCCCTGCCCC	TGCCAAAGCAAGCGCCCC	2300
Qy	2478	ATTGGAATTAAGATGGGGCTGGAGACATCTCTCTCTTCTGG	AGGCCAAAACCGGGCC	2537
Db	2301	ATTGGAATTAAGATGGGGCTGGAGACATCTCTCTCTTCTGG	AGGCCAAAACCGGGCC	2360
Qy	2538	CTCAGTTCCTCCAGGGTCAGCCTCCAGCGAGCTCTTCCCAAG	TGAGTCCCTCAGGT	2597
Db	2361	CTCAGTTCCTCCAGGGTCAGCCTCCAGCGAGCTCTTCCCAAG	TGAGTCCCTCAGGT	2420
Qy	2598	GGGCTCCTCCAGGTGGGCACAGAGCTGGCCCCCTCCCTGG	ATGGGAGGCTGGACCA	2657
Db	2421	GGGCTCCTCCAGGTGGGCACAGAGCTGGCCCCCTCCCTGG	ATGGGAGGCTGGACCA	2480
Qy	2658	GGAGGCTGAGGATCTGTCCGACTCCACCCACTTTGACGCGC	CTCAGAAACAGGTGAC	2717
Db	2481	GGAGGCTGAGGATCTGTCCGACTCCACCCACTTTGACGCGC	CTCAGAAACAGGTGAC	2540
Qy	2718	CATGCGCAAGTCTCCCTGGGTGGTCGGGGGCTACGACGGGT	TGGCTATGGCAC	2777
Db	2541	CATGCGCAAGTCTCCCTGGGTGGTCGGGGGCTACGACGGGT	TGGCTATGGCAC	2600
Qy	2778	CTTTGCGCTTTGGTGAGATGCAAGGGGCACTGTGGGGCAGG	GGGCCCATGTGGGCCAGGAT	2837
Db	2601	CTTTGCGCTTTGGTGAGATGCAAGGGGCACTGTGGGGCAGG	GGGCCCATGTGGGCCAGGAT	2660
Qy	2838	AGCTGGGCTGTGCTCCAGTCCGAGGAGGAGAGCAGGAGGAG	CGCCAGGCTGAGTCCCA	2897
Db	2661	AGCTGGGCTGTGCTCCAGTCCGAGGAGGAGAGCAGGAGGAG	CGCCAGGCTGAGTCCCA	2720
Qy	2898	GTCCGAGGAGCAGCAGGAGGCGCAGAGCCCATCTGCCAGGT	CAGTGCAGAGCC	2957
Db	2721	GTCCGAGGAGCAGCAGGAGGCGCAGAGCCCATCTGCCAGGT	CAGTGCAGAGCC	2780
Qy	2958	TGTGCTTGAGGTCCGACAGGCTCCCAACAGGAGCTCTCC	CAGAGCCACCCCATGGAGGA	3017
Db	2781	TGTGCTTGAGGTCCGACAGGCTCCCAACAGGAGCTCTCC	CAGAGCCACCCCATGGAGGA	2840
Qy	3018	CATCGGCGAGGTCTCCTCGTGAGATCCGGACCTGTTCAGGT	GTATGGGAGGCGGCCGA	3077
Db	2841	CATCGGCGAGGTCTCCTCGTGAGATCCGGACCTGTTCAGGT	GTATGGGAGGCGGCCGA	2900
Qy	3078	CACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACCT	CAACCTCTCAGACCTGTA	3137
Db	2901	CACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACCT	CAACCTCTCAGACCTGTA	2960
Qy	3138	CGATATCAGATACCTCCCATTCGAGTTTATGATCTTCAGGA	AAGTCCCAAGTCGGTCA	3197
Db	2961	CGATATCAGATACCTCCCATTCGAGTTTATGATCTTCAGGA	AAGTCCCAAGTCGGTCA	3020
Qy	3198	GCCAGAGCGGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCG	AGTTCCCGGAGCCCAAGTG	3257

[illegible]

Qy	4338	GCTGCGGAATACGAGGCCCTCAAGGGCTGCGCAACCCGACACTGCGCCAGTGCACGC	4397
Db	4161	GCTGCGGAATACGAGGCCCTCAAGGGCTGCGCAACCCGACACTGCGCCAGTGCACGC	4220
Qy	4398	AGCCTACTCAGCCCCCGGCACCTGGTGTCTCATCTTGGAGCTGTGTCTGGGCCCGAGCT	4457
Db	4221	AGCCTACTCAGCCCCCGGCACCTGGTGTCTCATCTTGGAGCTGTGTCTGGGCCCGAGCT	4280
Qy	4458	GCTCCCTGTGCTGGCCGAGAGGGCTCTCTACTCAGATCTTGAGTGAAGACTTACCTGTG	4517
Db	4281	GCTCCCTGTGCTGGCCGAGAGGGCTCTCTACTCAGATCTTGAGTGAAGACTTACCTGTG	4340
Qy	4518	GCAGATCTTGAGTGGCCACCCAGTACTCTGCACAAACAGCACATCTCTGCACCTGACCTGAG	4577
Db	4341	GCAGATCTTGAGTGGCCACCCAGTACTCTGCACAAACAGCACATCTCTGCACCTGAG	4400
Qy	4578	GTCGAGAAATGATCATCATCCGGAATACAACTCTGCTCAAGGTGCTGAGCCTGGCAATGC	4637
Db	4401	GTCGAGAAATGATCATCATCCGGAATACAACTCTGCTCAAGGTGCTGAGCCTGGCAATGC	4460
Qy	4638	ACAGAGCCTCAGCCAGGAGAAGTGTCTCCCTCAGACAAAGTTCAGGACTTACCTAGAGAC	4697
Db	4461	ACAGAGCCTCAGCCAGGAGAAGTGTCTCCCTCAGACAAAGTTCAGGACTTACCTAGAGAC	4520
Qy	4698	CATGGCTCCAGAGCTCCTCGAGGGCCAGGGGCTGTTCACAGACACACATCTGGGCGCAT	4757
Db	4521	CATGGCTCCAGAGCTCCTCGAGGGCCAGGGGCTGTTCACAGACACACATCTGGGCGCAT	4580
Qy	4758	CGTGTGACAGCTTTCATCATCTGAGCGCCGAGTACCCGGTGAAGCAGCAGAGGGTGCACG	4817
Db	4581	CGTGTGACAGCTTTCATCATCTGAGCGCCGAGTACCCGGTGAAGCAGCAGAGGGTGCACG	4640
Qy	4818	CGACTCTCAGAGAGGACTCGCACAGGGGTGGTCCGGCTGAGCCGCTGTCTACCGGGGCT	4877
Db	4641	CGACTCTCAGAGAGGACTCGCACAGGGGTGGTCCGGCTGAGCCGCTGTCTACCGGGGCT	4700
Qy	4878	GTCGCGGGGCGCGTGGCTTCTCTCGCAGACACTCTGTGCGCCACAGCCTTGGGGCCGCGC	4937
Db	4701	GTCGCGGGGCGCGTGGCTTCTCTCGCAGACACTCTGTGCGCCACAGCCTTGGGGCCGCGC	4760
Qy	4938	CTGCGCGTCCAGCTGTGCTCAGTGGCCGTGGCTAACAGAGAGGGGCCCGGCTGTTCGGG	4997
Db	4761	CTGCGCGTCCAGCTGTGCTCAGTGGCCGTGGCTAACAGAGAGGGGCCCGGCTGTTCGGG	4820
Qy	4998	GCCCGCGCCGTGACCTTCCCTACCGCGGGCTGGGTCTTCTGTCGCAATCGCAGAA	5057
Db	4821	GCCCGCGCCGTGACCTTCCCTACCGCGGGCTGGGTCTTCTGTCGCAATCGCAGAA	4880
Qy	5058	GAGACGGCGCTCTCTTACAGAGGCACAACCTGGCCGAGTGCCTGAGGGTTCGCCCGC	5117
Db	4881	GAGACGGCGCTCTCTTACAGAGGCACAACCTGGCCGAGTGCCTGAGGGTTCGCCCGC	4940
Qy	5118	GCCACACCTTGTCTCCCGTGGGGTTCGCTCAGACGCGCCAAATAAAACGCACAGC	5177
Db	4941	GCCACACCTTGTCTCCCGTGGGGTTCGCTCAGACGCGCCAAATAAAACGCACAGC	5000
Qy	5178	CGGCGGA	5184
Db	5001	CGGCGGA	5007

RESULT 7

RESUL1)
AAC62287
ID AAC62287 standard; cDNA; 7928 BP.

AAC62287;

XX
DT 19-MAR-2001 (first entry)

XX CDNA encoding a splice variant of a signal transduction polypeptide.

XX
KW Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;

congestive heart failure; dilated congestive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis; arteriosclerosis; cardiac tumour; microbial infection; spicule variant; ss.

OS Homo sapiens.

AA	Key	Location/Qualifiers
FF	CDS	60. .7850
FT		

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FT      /product= "signal transduction polypeptide H19G5 splice  
FT      variant"
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PN WO2000063381-A1.

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PD
26-000-2000

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[illegible]

FA (SCIO-) SCIOS INC.
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Zeng W, Stanton L, Kong H;
PI
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WPI; 2001-007013/01.
D. DDD. 20020500

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exhibiting kinase activity useful for identifying antibodies to treat

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catalytic diseases, and structural and functional changes in the
transduction.

CLAIM 4; Page 65-66; 8TBP; English.
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The present sequence encodes a splice variant of human in signal transduction polypeptide. The polypeptide is designated H1005. The

protein is capable of regulating signal transduction and exhibits kinase

CC polypeptides and polynucleotides are useful for preventing or treating a

CC cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,

CC mitral valve disease, aortic valve disease or tricuspid valve disease,
CC angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,

arterial or renovascular hypertension, arteriosclerosis, atherosclerosis and cardiac tumours in humans. The polypeptide is also useful for

detecting the expression of a protein capable of regulating signal

CC or acceptor molecule of a phosphate group. The monoclonal antibodies can

cell samples, and therefore used in humans for localization and

cc
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Monitoring of Microbial Infection
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Sequence 7928 BP; 1535 A; 2644 C; 2488 G; 1261 T; 0 U; 0 Other;

Query Match	Score 4915.8; DB 5; Length 7928;
Best Local Similarity	94.4%;
Best NCBI Similarity	94.4%;
Best NCBI Similarity	94.4%;

Matches 4920; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 258 CCCAGGGCCCCCATCCATGCAGGTAACCATCGAGGATGTCAGGCACAGACAGGCGGAAC 317

Db 3002 CGACGGCCCCATCCATGCAGGTAAACCATCGAGGATGTGCAGGCACAGACAGCGGAAC 3061

318 GGCCCAATTTCGAGGCTATCATTTAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAGGA 377

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[illegible]

QY 438 CCIGGCGTGGAGGCATGTGCGCCCTCAGAAAGGAATGCCGACCTTACACCTTCGCCCTCGCCCAAAA 439

[REDACTED]

3182	CTGTGGTCTGAGCATGTGGCTCTGAAGATGCGGGCGTTATACACCTGCGCTGGCCCAAA	3241
498	CATGTGGCCAGGTGCTCTGCAAGGCAAGAGCTGCTGTGTTCTGGGGGGACAAATGAGCC	557
3242	CACGTGGGCCAGGTGCTCTGCAAGGCGAAGCTGCTGTGTCTTGGGGGGACAAATGAGCC	3301
558	GGACTCAGAGAAGCAAAAGCCACCGAGGAAGCTGCATCTCTTCATCAGAGTCAAGAGGA	617
3302	GGACTCAGAGAGCAAAAGCCACCGAGGAAGCTGCATCTCTTCATCAGGTCAAGGAGGA	3361
618	GATTGGAAGGGGGTGTGTTGGCTTCGTTAAAAGAGTGCAGCAAAAAGAAACAGATCTT	677
3362	GATTGGAAGGGGGTGTGTTGGCTTCGTTAAAAGAGTGCAGCAAAAAGAAACAGATCTT	3421
678	GTGCGCTGCCAAGTTTCATCCCTCTACGGAGCAGAACTCGGGCCGAGGCATACAGGGAGCG	737
3422	GTGCGCTGCCAAGTTTCATCCCTCTACGGAGCAGAACTCGGGCCGAGGCATACAGGGAGCG	3481
738	AGACATCTGGCCGCGCTGAGCCACCGCTGGTCAACGGGGCTGTGCACCAAGTTTGAGAC	797
3482	AGACATCTGGCCGCGCTGAGCCACCGCTGGTCAACGGGGCTGTGCACCAAGTTTGAGAC	3541
798	CCGCAAGAACCCTCATCCTCATCTGGAGCTGTGCTCATCCGAGGAGTGTGTCACGCGCT	857
3542	CCGCAAGAACCCTCATCCTCATCTGGAGCTGTGCTCATCCGAGGAGTGTGTCACGCGCT	3601
858	GTACAGGAAGGGCGTGGTCAACGGAGCCGAGGTCAAGTCTACATCCAGCAGCTGTGGA	917
3602	GTACAGGAAGGGCGTGGTCAACGGAGCCGAGGTCAAGTCTACATCCAGCAGCTGTGGA	3661
918	GGGCTGCACTACCTGCACAGGCATCGGCTTCTCCACTGGACATAAAGCCCTCTAACAT	977
3662	GGGCTGCACTACCTGCACAGGCATCGGCTTCTCCACTGGACATAAAGCCCTCTAACAT	3721
978	CTGTAGTGGTGATCTGCCCCGGGAGACATTAAATCTGGAGCTTTGGCTTTGCCAGAA	1037
3722	CTGTATGGTGCATCTCTGCCCGGAAGACATTAAATCTGGAGCTTTGGCTTTGCCAGAA	3781
1038	CATCACCCCAGCAGAGCTGCAATTCAGCCAGTACGGCTCCCTGAGTTCCTCTCCCCCGA	1097
3782	CATCACCCCAGCAGAGCTGCAATTCAGCCAGTACGGCTCCCTGAGTTCCTCTCCCCCGA	3841
1098	GATCATCCAGCAGAACCCCTGTGAGCGAAGCTCCGACATTTGGGCCATGGTGTCACTCTC	1157
3842	GATCATCCAGCAGAACCCCTGTGAGCGAAGCTCCGACATTTGGGCCATGGTGTCACTCTC	3901
1158	CTACCTCAGCTGACCTGTCTCATCCCAATTTGCCGGGAGAGTGACCGTGCCACCTTCCT	1217
3902	CTACCTCAGCTGACCTGTCTCATCCCAATTTGCCGGGAGAGTGACCGTGCCACCTTCCT	3961
1218	GACGCTCTGGAGGGCGGTGTCATGAGCAGAGCCCATGCTGCCACCTCAGCGAAGA	1277
3962	GACGCTCTGGAGGGCGGTGTCATGAGCAGAGCCCATGCTGCCACCTCAGCGAAGA	4021
1278	CGCCAAAGATTCATCAAGGCTACGCTCGAGAGAGCCCTCAGGCCCGGCTATATGGGCG	1337
4022	CGCCAAAGATTCATCAAGGCTACGCTCGAGAGAGCCCTCAGGCCCGGCTATATGGGCG	4081
1338	CCAGTGCTCTCCACCCCTGGTTCTGAAATCCATGCTCGGAGAGAGCCCACTTCAT	1397
4082	CCAGTGCTCTCCACCCCTGGTTCTGAAATCCATGCTCGGAGAGAGCCCACTTCAT	4141
1398	CAACACCAAGCAGCTCAAGTTCTCTCGCCGGAAGTGCCTGGAGAGGTTCCCTGTATGAG	1457
4142	CAACACCAAGCAGCTCAAGTTCTCTCGCCGGAAGTGCCTGGAGAGGTTCCCTGTATGAG	4201
1458	CTCAAGTCCATCCTGGTGAATGCGTCCATCCCTGAGCTGTGGGGGGCCACCCGACAG	1517
4202	CTCAAGTCCATCCTGGTGAATGCGTCCATCCCTGAGCTGTGGGGGGCCACCCGACAG	4261
1518	CCCTCCCTCGGCGTAGCCCGGCACTCTGAGAGGACAATGGTGGCTCTTCAGTTCCTC	1577
4262	CCCTCCCTCGGCGTAGCCCGGCACTCTGAGAGGACAATGGTGGCTCTTCAGTTCCTC	4321

[illegible][illegible]

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Example 1: Page 204-205: 218pp: English.

The invention provides human protein kinases and protein kinase-like enzymes and polynucleotides encoding the polypeptides. The kinase polypeptides and their modulators are useful for treating a disease or disorder such as cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders, and organ transplant rejection. They are also useful for treating rhinitis, autoimmunity, atherosclerosis, psoriasis, osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic inflammatory bowel disease, rheumatoid arthritis, metabolic disorders such as diabetes, obesity, cardiovascular diseases such as reperfusion injury, coronary thrombosis, clotting disorders and atherosclerosis, ocular diseases such as glaucoma, retinopathy and macular degeneration, psychiatric and neurological disorders such as anxiety, schizophrenia, dementia, manic depression, etc. The polynucleotides are useful in gene therapy techniques to treat the above mentioned disorders. Sequences AAH46891-46922 represent human protein kinases encoding cDNA molecules

Sequence 4936 BP; 923 A; 1695 C; 1524 G; 794 T; 0 U; 0 Other;

93.8%; Score 4885.2; DB 4; Length 4936;

Model	Local Similarity	Pred. No. 0;	Indels	Gaps
Conservative	99.6%	0	3	18
Mismatches 4915				

268 CCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCCGAACGGCCCCAATTC 327

1 CCATCCATGCAGGTAAACCATCGAGGATGTGCAGGCACAGACAGGCCAATC 60

328 GAGGCTATCATTGAGGGGACCCACAGCCCTCGGTGACCTGGTACAGGACAGCGTCCAG 387

100

61 GAGGCTATCATGTGAGGCGACCCACAGCCCTCGTGACCTGGTACAAGGACAGCGTCCAG 120

388 CTGGTGACAGCACCCGGCTTAGCCAGCAGCAAGAGGACCACTACTCCCTGGTGCTG 447

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121 CTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAGGCACCACTAC'TCCC'TGGTGC'TG 180

448 AGGCATGTGGCCTCGAAGGATGCCGGCGGTTACACCTGCCTGGCCCAAACACTGGTGGC 507

[illegible][illegible]

508 CAGGTGCTCTGCAAGGCAGAGCTGCTGGTGGTCTTGGG-----GGGGAC 549

241 CAGGTGCTCTGCACAGGCCAGGACTGGTGGTGCTGGCGCCGCTTCCTCCTCCTTACGGGAC 300

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550 AATGAGCCGACTCAGAGAAGCAAGCCACCGAGGAAGCTCCTTCTATGAGGTC 609

301 AATGAGCCGGACTCAGAGAGCAAGCCACCGGAGGAAGCTGCACTCCTTCATGAGGTC 360

QUESTION

610 AAGGAGGAGATTGGAAAGGGCGTGTTCGGCTTCGTAAAGAGTGCAGCACAAAGGAAAC 669

361 AAGCAGGAGATTGGAAGGGCGTGTTGGCTTCGTAAAGAGTGCAGCAAGGAAAC 420

670 AAGATCTTGTGCGCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATAC 729

421 AAGATCTTGTGCGCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATAC 480

730 AGGGAGCGAGACATCTGGCCCGCTGAGCCACCCCGCTGGTACGGGGCTGCTGGACCAG 789

481 AGGGAGCGAGACATCCTGGCCGCGCTGAGCCACCCGCTGGTCAAGGGGCTGCTGGACCAAG 540

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790 TTGTGAGACCCGCAAGACCCCTCATCTCTGGAGCTGTGCTCATCCGAGGAGCTGCTG 849

542 TTTGAGACCCGCAAGACCCCTCATCTCATCTGGAGCTGTGCTCATCCGAGGAGCTGCTG 600

Qy	850	GACGCGCTGTACAGGAAGGGCGTGGTGA	CGGAGGCCGAGTCAAGTCTACATCCAGCAG	909
Db	601	GACGCGCTGTACAGGAAGGGCGTGGTGA	CGGAGGCCGAGTCAAGTCTACATCCAGCAG	660
Qy	910	CTGGTGGAGGGGCTGCACCTACCTGCAC	AGCCATGGGCTTCTCCACCTGGACATAAAGCCC	969
Db	661	CTGGTGGAGGGGCTGCACCTACCTGCAC	AGCCATGGGCTTCTCCACCTGGACATAAAGCCC	720
Qy	970	TCTAAACATCTGATGGTGCACTCTGCGCC	GGGAAGACATTAATAATCTGCACCTTTTGCGTTT	1029
Db	721	TCTAAACATCTGATGGTGCACTCTGCGCC	GGGAAGACATTAATAATCTGCACCTTTTGCGTTT	780
Qy	1030	GCCCAGAAATCAACCCAGCAGAGCTGCA	GTTGAGCCAGTACGGCTCCCTGAGTTCGTG	1089
Db	781	GCCCAGAAATCAACCCAGCAGAGCTGCA	GTTGAGCCAGTACGGCTCCCTGAGTTCGTG	840
Qy	1090	TCCCCGAGATCATCCAGCAGAAACCTCT	GTGAGCGAAGCCTCGACATTTTGGGCGCATGGGT	1149
Db	841	TCCCCGAGATCATCCAGCAGAAACCTCT	GTGAGCGAAGCCTCGACATTTTGGGCGCATGGGT	900
Qy	1150	GTCACTCTCTACCTCAGCCTGACCTGCT	CATCCCCATTTGCCGGCGAGAGTACCCGTGCC	1209
Db	901	GTCACTCTCTACCTCAGCCTGACCTGCT	CATCCCCATTTGCCGGCGAGAGTACCCGTGCC	960
Qy	1210	ACCTCTCTGAACGTCTGAGAGGGCGGTGT	CATGAGCGAGCCCATGGCTGCGCACCTC	1269
Db	961	ACCTCTCTGAACGTCTGAGAGGGCGGTGT	CATGAGCGAGCCCATGGCTGCGCACCTC	1020
Qy	1270	AGGGAAGACGCCAAAGACTTCATCAAG	GGCTACGCTGCAGAGAGCCCTCAGGCCCCGGCCT	1329
Db	1021	AGGGAAGACGCCAAAGACTTCATCAAG	GGCTACGCTGCAGAGAGCCCTCAGGCCCCGGCCT	1080
Qy	1330	AGTGGCGCCAGTGCTCTCCCAACCTTGG	TCTGAAATCCATGCTCGGAGGAGGGCC	1389
Db	1081	AGTGGCGCCAGTGCTCTCCCAACCTTGG	TCTGAAATCCATGCTCGGAGGAGGGCC	1140
Qy	1390	CACCTTCATCAACACCAAGCAGCTCA	AGTTCTCTCTGGCCCGAAGTCCGTGGCAGCGTTCC	1449
Db	1141	CACCTTCATCAACACCAAGCAGCTCA	AGTTCTCTCTGGCCCGAAGTCCGTGGCAGCGTTCC	1200
Qy	1450	CTGATGAGCTTACAGTCCATCTCTGGT	GATGCGCTCCATCCCTCAGCTGCTGCGGGGCCCA	1509
Db	1201	CTGATGAGCTTACAGTCCATCTCTGGT	GATGCGCTCCATCCCTCAGCTGCTGCGGGGCCCA	1260
Qy	1510	CCGACAGCCCCCTCCCTCGCGTAGCC	CGGCACTCTGACGAGACACTGGTGGCTCCTCC	1569
Db	1261	CCGACAGCCCCCTCCCTCGCGTAGCC	CGGCACTCTGACGAGACACTGGTGGCTCCTCC	1320
Qy	1570	AGTTCTCTCTCTCTGTGACAAACAG	AGCTCGCCCCATTTGCCGGGCTAAAGTCACTGGCCA	1629
Db	1321	AGTTCTCTCTCTCTGTGACAAACAG	AGCTCGCCCCATTTGCCGGGCTAAAGTCACTGGCCA	1380
Qy	1630	CCCTCCCGGTGACACACTCAACACT	CGCTGCAACCCCGGGGCTTCTGCGGCCCTCGGCC	1689
Db	1381	CCCTCCCGGTGACACACTCAACACT	CGCTGCAACCCCGGGGCTTCTGCGGCCCTCGGCC	1440
Qy	1690	AGCTGCTCTGAGAAAGCCGAGGCGCT	GAGCGCTCCACCGAGGCCCGCAGCTCCGCTGCA	1749
Db	1441	AGCTGCTCTGAGAAAGCCGAGGCGCT	GAGCGCTCCACCGAGGCCCGCAGCTCCGCTGCA	1500
Qy	1750	TCTCCGAGGGTGC	CGGGGCCACCGGGCTGCGTGGCCCCCGGCACACGCTCATC	1809
Db	1501	TCTCCGAGGGTGC	CGGGGCCACCGGGCTGCGTGGCCCCCGGCACACGCTCATC	1560
Qy	1810	CGCAGCTGTCTTACACACAGGGCGGT	GAGAGCCCTGAGCACGGGGCCCTTGGCCCCCGGG	1869
Db	1561	CGCAGCTGTCTTACACACAGGGCGGT	GAGAGCCCTGAGCACGGGGCCCTTGGCCCCCGGG	1620
Qy	1870	AGCAGCGGCACCGGGCCCGCGCGGC	ACCTGCTGAAGGGCGGCTACATTTGGGGGGCG	1929
Db	1621	AGCAGCGGCACCGGGCCCGCGCGGC	ACCTGCTGAAGGGCGGCTACATTTGGGGGGCG	1680
Qy	1930	CTGCCAGGCGTGGCGGAGGCACCTG	ATGAGGACCCGGCTGCTGGAGAGGAGGCGCGCAG	1989

1681	Db		CTGCGAGGCCCTGCGCGAGGCCACTGATGGAGACACGCGTGCTGGAGGAGGAGCGCGCCAGG	1740
1990	QY		GAGGAGCAGGCCACCCCTCTCTGGCCAAAGCCCTCATTTGAGACTGCCCTCCGGCTGCCT	2049
1741	Db		GAGGAGCAGGCCACCCCTCTCTGGCCAAAGCCCTCATTCGAGACTGCCCTCCGGCTGCCT	1800
2050	QY		GCCTCTGSCACCGACTTGGGCCCTTGCCACAGCCACTCCCTGGAACATGACTCTCGAGC	2109
1801	Db		GCCTCTGSCACCCCACTTGGGCCCTTGCCACAGCCACTCCCTGGAACATGACTCTCGAGC	1860
2110	QY		ACCCGCCGCCCTCTCTCGGAGGCGCTCGGTTGAGGCACAGCAGCTGCCCTCAGCCCCCTCC	2169
1861	Db		ACCCGCCGCCCTCTCTCGGAGGCGCTCGGTTGAGGCACAGCAGCTGCCCTCAGCCCCCTCC	1920
2170	QY		GGGGGGCCCCATCAGGGACATGGGGCACCTTCAGGGCTCCACAGCAGCTTCATCCACT	2229
1921	Db		GGGGGGCCCCATCAGGGACATGGGGCACCTTCAGGGCTCCACAGCAGCTTCATCCACT	1980
2230	QY		GGTGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCTTGGGGCAG	2289
1981	Db		GGTGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCTTGGGGCAG	2040
2290	QY		CCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCGCAGGAGGGCTGCAGCCCCAC	2349
2041	Db		CCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCGCAGGAGGGCTGCAGCCCCAC	2100
2350	QY		CCAGCAGTGTCCCCTCTCTGCTCTCTTCCCTCCAGGACTGTGCAAGAGGCCCCC	2409
2101	Db		CCAGCAGTGTCCCCTCTCTGCTCTCTTCCCTCCAGGACTGTGCAAGAGGCCCCC	2160
2410	QY		TTAGTACCCCTCAAGCCCTTCTTTGGACAGCCCCCAGGCACCCCTGCCCTGCCAAGCA	2469
2161	Db		TTAGTACCCCTCAAGCCCTTCTTTGGACAGCCCCCAGGCACCCCTGCCCTGCCAAGCA	2220
2470	QY		AGCCCCCAATTGGACTCTAAGATGGGGCTTGAGAGACTCTCTCTTCTGGGAGGCCAAAA	2529
2221	Db		AGCCCCCAATTGGACTCTAAGATGGGGCTTGAGAGACTCTCTCTTCTGGGAGGCCAAAA	2280
2530	QY		CCGGCCCTCTCAGTCTCCACAGGTCAGCTCTCCAGGGGAGCTCTTCCCAAGTCAGCTCC	2589
2281	Db		CCGGCCCTCTCAGTCTCCACAGGTCAGCTCTCCAGGGGAGCTCTTCCCAAGTCAGCTCC	2340
2590	QY		CTCAGGTTGGCTCCTTCCCAGTTGGGCACAGAGCTTGGCCCTCCCTGGATGGGAGGGC	2649
2341	Db		CTCAGGTTGGCTCCTTCCCAGTTGGGCACAGAGCTTGGCCCTCCCTGGATGGGAGGGC	2400
2650	QY		TGAGCCACGAGGCTGAGGATCTGTCCGACTCCACACCACTTGCAGCGGCTTCAGGAA	2709
2401	Db		TGAGCCACGAGGCTGAGGATCTGTCCGACTCCACACCACTTGCAGCGGCTTCAGGAA	2460
2710	QY		CAGTGACCATGSCCAAGTTCTCCCTGGGTGTGCGGGGGCTACGACGGCTGGCTGGC	2769
2461	Db		CAGTGACCATGSCCAAGTTCTCCCTGGGTGTGCGGGGGCTACGACGGCTGGCTGGC	2520
2770	QY		TATGSCACTTTTGCTTTTGGTGAGATGACAGGGGGATGCTTGGGGCAGGGGCCCATGTGG	2829
2521	Db		TATGSCACTTTTGCTTTTGGTGAGATGACAGGGGGATGCTTGGGGCAGGGGCCCATGTGG	2580
2830	QY		GCACGATAGCCTTGGGCTGTGTCCCACTCGAGTGGAGAGAGAGAGAGGAGGCCCAGGGCT	2889
2581	Db		GCACGATAGCCTTGGGCTGTGTCCCACTCGAGTGGAGAGAGAGAGAGAGGAGGCCCAGGGCT	2640
2890	QY		GAGTCCCACTCGAGGAGCAGCAGGAGGCCAGGGCTGAGGCCACCTGCCCCAGGTCAGT	2949
2641	Db		GAGTCCCACTCGAGGAGCAGCAGGAGGCCAGGGCTGAGGCCACCTGCCCCAGGTCAGT	2700
2950	QY		GCAAGGCTGTGCTGAGTTGGCAGAGGGCTCCCAACAGGAGCTCTCAGAGCCACCCCA	3009
2701	Db		GCAAGGCTGTGCTGAGTTGGCAGAGGGCTCCCAACAGGAGCTCTCAGAGCCACCCCA	2760
3010	QY		TGGAGGACATCGGGCAGGCTCTCCCTGGTGCAGATCCGGGACCTGTCTCAGTGTATGCGGAG	3069

2761	DB	TGGAGGACATCGGAGAGGTCTCCCTGTGTGCAGATCCGGGACCTGTCAAGTGATCGGGAG	28220
3070	QY	GGGGCGGACACAATATTCCTTGACATTTTCGAGGTGGACCCCGCCTACTCAACCTCTCA	3129
2821	DB	GGGGCGGACACAATATTCCTTGACATTTTCGAGGTGGACCCCGCCTACTCAACCTCTCA	2880
3130	QY	GACCTGTACGATATCAGGTACCTCCCATTCGAGTTTATGATCTTCAGGAAGTCCCCCAAG	3189
2881	DB	GACCTGTACGATATCAGGTACCTCCCATTCGAGTTTATGATCTTCAGGAAGTCCCCCAAG	2940
3190	QY	TCCGCTAGCCAGACGCGCCCTCCCCCATTTGGTGTAGGAGGAGCTGGCCGAGTTCCTCGGAG	3249
2941	DB	TCCGCTAGCCAGACGCGCCCTCCCCCATTTGGTGTAGGAGGAGCTGGCCGAGTTCCTCGGAG	3000
3250	QY	CCCAGTGGCCCTGGCCAGGTGAACTGGGCCCCCAACGACGGGCTTGAGATCACAGAGGAG	3309
3001	DB	CCCAGTGGCCCTGGCCAGGTGAACTGGGCCCCCAACGACGGGCTTGAGATCACAGAGGAG	3060
3310	QY	TACAGAGATGTGGACGCGCTGTGTGGAGAGGTGCGCTGGGAGAGAACGCAAGTGTGTCC	3369
3061	DB	TACAGAGATGTGGACGCGCTGTGTGGAGAGGTGCGCTGGGAGAGAACGCAAGTGTGTCC	3120
3370	QY	TGCGCGTACGACGAGCTCTTCCACTTCCTGGGAGGCACCTGCCCTGGATGAGCGCTGCA	3429
3121	DB	TGCGCGTACGACGAGCTCTTCCACTTCCTGGGAGGCACCTGCCCTGGATGAGCGCTGCA	3180
3430	QY	GAGCTGGGGCTCGGTGAGAGATGAAGGCTTCGTTGGAGACATCTCCCGGATCTCTGAAG	3489
3181	DB	GAGCTGGGGCTCGGTGAGAGATGAAGGCTTCGTTGGAGACATCTCCCGGATCTCTGAAG	3240
3490	QY	GGCAGGCCCGAAGGTCTTGAGAAAGAGGGGGCCCCCAGGAAGAACCCAGGCGCTTCTTCC	3549
3241	DB	GGCAGGCCCGAAGGTCTTGAGAAAGAGGGGGCCCCCAGGAAGAACCCAGGCGCTTCTTCC	3300
3550	QY	TTCCGGCTCTCAGGTCGAGAGCTGGAGACGAGGCCCGACATCTCTTAAGGGAGCTCTCA	3609
3301	DB	TTCCGGCTCTCAGGTCGAGAGCTGGAGACGAGGCCCGACATCTCTTAAGGGAGCTCTCA	3360
3610	QY	GATGAGACTGTGGTCTCGGGCCAGTCAGTGACATCTGGCTTCGCAAGTGTCAAGCCAGCCA	3669
3361	DB	GATGAGACTGTGGTCTCGGGCCAGTCAGTGACATCTGGCTTCGCAAGTGTCAAGCCAGCCA	3420
3670	QY	GCTGCCAGGCCACTCGTAGCMAAGACGGAGCCCGCTGGAGAGCAGACGGTGTCTCTC	3729
3421	DB	GCTGCCAGGCCACTCGTAGCMAAGACGGAGCCCGCTGGAGAGCAGACGGTGTCTCTC	3480
3730	QY	ATCTCTGCCACCCTCAAGAACTTCACAGCTTCTGACCATCTCTGGTGGTGGTGGAGGAC	3789
3481	DB	ATCTCTGCCACCCTCAAGAACTTCACAGCTTCTGACCATCTCTGGTGGTGGTGGAGGAC	3540
3790	QY	CTGGGTGTGTACCTGTGAGCGTGTAGCAATGGCGTGGGGACAGTGACACCAACCGGCGTC	3849
3541	DB	CTGGGTGTGTACCTGTGAGCGTGTAGCAATGGCGTGGGGACAGTGACACCAACCGGCGTC	3600
3850	QY	CTCCGAAAGGACAGCGCGCCCTCATCTTCGCCATCGCCCGATATCGGGAGAGGTGTACCGG	3909
3601	DB	CTCCGAAAGGACAGCGCGCCCTCATCTTCGCCATCGCCCGATATCGGGAGAGGTGTACCGG	3660
3910	QY	GATGGGTGCTGTGGTCTGGAGCCGTTGGAACTCTACGGCCCTGTGACCTACATCTGTG	3969
3661	DB	GATGGGTGCTGTGGTCTGGAGCCGTTGGAACTCTACGGCCCTGTGACCTACATCTGTG	3720
3970	QY	CAGTGCAGCCTAAGAGGGCGAGCTGGACCACACTGGCCTCCGACATCTTTGACTGTGTC	4029
3721	DB	CAGTGCAGCCTAAGAGGGCGAGCTGGACCACACTGGCCTCCGACATCTTTGACTGTGTC	3780
4030	QY	TACCTGACCAAGCTCTCCCGGGTGGACCTACACTTTCGACCGGCACTGTGTGACG	4089
3781	DB	TACCTGACCAAGCTCTCCCGGGTGGACCTACACTTTCGACCGGCACTGTGTGACG	3840
4090	QY	AAGGAGGAATGGGTCTCTACAGCAGCCCTCGGAGCAAGTCTCTCGGAGGGGCCACG	4149
3841	DB	AAGGAGGAATGGGTCTCTACAGCAGCCCTCGGAGCAAGTCTCTCGGAGGGGCCACG	3900

QY 4150 CACTGCTCTCAGGAGGAGGAGCCAGGGGCGGTGAGCCCAACCCCTGCCCGACAAAG 4209
Db 3901 CACTGCTCTCAGGAGGAGGAGCCAGGGGCGGTGAGCCCAACCCCTGCCCGACAAAG 3960
QY 4210 ACTTTCGATTCAGACACAGATTCAGAGGGGCGGCTTCAGCGTGGTGGCAATGCTGG 4269
Db 3961 ACTTTCGATTCAGACACAGATTCAGAGGGGCGGCTTCAGCGTGGTGGCAATGCTGG 4020
QY 4270 GAGAAGGCCAGGGGCGGCTTGGCGGCAAGATCATCCCTACCAACCCCAAGGACAAG 4329
Db 4021 GAGAAGGCCAGGGGCGGCTTGGCGGCAAGATCATCCCTACCAACCCCAAGGACAAG 4080
QY 4330 ACAGCAGTGTGCGGCAATACAGAGGCTTCAGAGGCGCTTGGCGGCAACCTGGCCAG 4389
Db 4081 ACAGCAGTGTGCGGCAATACAGAGGCTTCAGAGGCGCTTGGCGGCAACCTGGCCAG 4140
QY 4390 CTGACGACGCTTACCTCAGCGCCCGGCAACCTGGGCTCATCTTGGAGCTGTGCTCTGG 4449
Db 4141 CTGACGACGCTTACCTCAGCGCCCGGCAACCTGGGCTCATCTTGGAGCTGTGCTCTGG 4200
QY 4450 CCGAGCTGTCTCCCTGCTGCGGAGGAGGCTCTCTACTCAGATCTGAGGTGAAGGAC 4509
Db 4201 CCGAGCTGTCTCCCTGCTGCGGAGGAGGCTCTCTACTCAGATCTGAGGTGAAGGAC 4260
QY 4510 TACCTGTGGCAGATGTGAGTGTGCGGCAACCTGCTGCAACCCAGCAGATCTGCACTG 4569
Db 4261 TACCTGTGGCAGATGTGAGTGTGCGGCAACCTGCTGCAACCCAGCAGATCTGCACTG 4320
QY 4570 GACCTGAGTCCGAGACATGATCATCCGATACACCTGCTCAAGGTCTGAGGCTG 4629
Db 4321 GACCTGAGTCCGAGACATGATCATCCGATACACCTGCTCAAGGTCTGAGGCTG 4380
QY 4630 GGCATGCAAGAGCTCAGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4689
Db 4381 GGCATGCAAGAGCTCAGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4440
QY 4690 CTAGAGACATGCTCCAGAGCTCTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 4749
Db 4441 CTAGAGACATGCTCCAGAGCTCTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 4500
QY 4750 TGGGCAATGCTGTGACAGCTTCTGCTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTG 4809
Db 4501 TGGGCAATGCTGTGACAGCTTCTGCTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTG 4560
QY 4810 GGTGCAAGGAGCTGAGAGGAGCTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 4869
Db 4561 GGTGCAAGGAGCTGAGAGGAGCTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 4620
QY 4870 GCGGAGCTGTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4929
Db 4621 GCGGAGCTGTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4680
QY 4930 GCGGAGCTGTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4989
Db 4681 GCGGAGCTGTGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4740
QY 4990 TGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5049
Db 4741 TGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4800
QY 5050 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5109
Db 4801 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4860
QY 5110 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5169
Db 4861 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4920
QY 5170 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5185
Db 4921 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4936

RESULT 9
AAC62285
ID AAC62285 standard; cDNA; 4175 BP.
XX
AC AAC62285;
XX
DT 19-MAR-2001 (first entry)
XX
cDNA encoding a human signal transduction polypeptide.
DE
XX
XX
KW Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
congestive heart failure; dilated congestive cardiomyopathy;
KW hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KW mitral valve disease; aortic valve disease; tricuspid valve disease;
KW myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW atherosclerosis; cardiac tumour; microbial infection; ss.
XX
OS Homo sapiens.
XX
XX
PH Key Location/Qualifiers
FT CDS 1..4056
FT /*tag= a
FT /product= "signal transduction polypeptide H19G5"
XX
PN WO200063381-A1.
XX
PD 26-OCT-2000.
XX
XX
PF 11-APR-2000; 2000WO-US009488.
XX
XX
PR 16-APR-1999; 99US-0129553P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Zeng W, Stanton L, Kong H;
XX
XX WPI: 2001-007013/01.
XX P-PSDB; AAB30567.
XX
PT Novel h19G5 polypeptides capable of regulating signal transduction and
exhibiting kinase activity useful for identifying antibodies to treat
cardiac diseases, and additional mediators of signal transduction.
XX
PS Claim 4; Page 57-59; 81pp; English.
XX
XX The present sequence encodes a human protein with putative function in
signal transduction. The polypeptide is designated H19G5. The protein is
capable of regulating signal transduction and exhibits kinase activity.
XX The H19G5 transcript is expressed in the heart. H19G5 polypeptides and
polynucleotides are useful for preventing or treating a cardiac disease,
XX such as congestive heart failure, dilated congestive cardiomyopathy,
XX hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve
XX disease, aortic valve disease or tricuspid valve disease, angina
XX pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial
XX or renovascular hypertension, arteriosclerosis, atherosclerosis and
XX cardiac tumours in humans. The polypeptide is also useful for detecting or
XX the expression of a protein capable of regulating signal transduction or
XX the expression of a protein capable of acting as a donor or acceptor
XX molecule of a phosphate group. The monoclonal antibodies can be used as
XX probes for detecting discrete antigens expressed by tissue or cell
XX samples, and therefore used in humans for localization and monitoring of
XX microbial infection
XX
SQ Sequence 4175 BP; 778 A; 1459 C; 1283 G; 655 T; 0 U; 0 Other;
Query Match 79.8%; Score 4146.6; DB 5; Length 4175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4149; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1055 TGCAGTTCAGCCAGTACGGCTCCCTGAGTTCGCTCCCGGAGATCATCCAGAGAAC 1114
Db 5 TGCAGTTCAGCCAGTACGGCTCCCTGAGTTCGCTCCCGGAGATCATCCAGAGAAC 64

2195	QY	GGCACTCTCAGGGGTCAAAGCAGCTTCCATCCATCTGTGTGGCCACCCAGAGCATGTCTCAGC	2254
1145	DB	GGCACTCTCAGGGGTCAAAGCAGCTTCCATCCATCTGTGTGGCCACCCAGAGCATGTCTCAGC	1204
2255	QY	CAGAGAGCCCATCCCGGACAGCCCTTTGGGGGACAGCCAGCCCCCTTTCTGGCACCCCAAGC	2314
1205	DB	CAGAGAGCCCATCCCGGACAGCCCTTTGGGGGACAGCCAGCCCCCTTTCTGGCACCCCAAGC	1264
2315	QY	AGGGTCTGTGCCCCCAGAGAGGGCTGACGCCCCACCCAGCAGTTGCCCCCATGCCCTCCTG	2374
1265	DB	AGGGTCTGTGCCCCCAGAGAGGGCTGACGCCCCCCAGCAGTTGCCCCCATGCCCTCCTG	1324
2375	QY	GCTCTTTCCTCCAGGANTTTGAAAGAGGCCCCCTTAGTACCTCCAAAGCCCCCTTTCTTGG	2434
1325	DB	GCTCTTTCCTCCAGGANTTTGAAAGAGGCCCCCTTAGTACCTCCAAAGCCCCCTTTCTTGG	1384
2435	QY	GACAGCCCCAGGACGCCCTTGCCCTTGCCAAAGAACGCCCCCATTCGGAATCTAAAGATGG	2494
1385	DB	GACAGCCCCAGGACGCCCTTGCCCTTGCCAAAGAACGCCCCCATTCGGAATCTAAAGATGG	1444
2495	QY	GGCTGTGAGACATCTCTTCTCTGGAGGCGCANAACCCGGCCCCCTGCAGTTCCCAAGGT	2554
1445	DB	GGCTGTGAGACATCTCTTCTCTGGAGGCGCANAACCCGGCCCCCTGCAGTTCCCAAGGT	1504
2555	QY	CAGCTCTCCAGGCGAGCTCTTCCCAAGTAGCTCCCTCAGGGTGGGCTCTCCCAAGGTGG	2614
1505	DB	CAGCTCTCCAGGCGAGCTCTTCCCAAGTAGCTCCCTCAGGGTGGGCTCTCCCAAGGTGG	1564
2615	QY	GCACAGAGCTGGCCCCCTCCCTGGATGCGAGGGCTGGACCCAGAGGCTGAGATCTGT	2674
1565	DB	GCACAGAGCTGGCCCCCTCCCTGGATGCGAGGGCTGGACCCAGAGGCTGAGATCTGT	1624
2675	QY	CCGACTCCACACCCTTGACGCGCTCTCAGGAACAGGTGACCATGCGCAAGTTCTCCC	2734
1625	DB	CCGACTCCACACCCTTGACGCGCTCTCAGGAACAGGTGACCATGCGCAAGTTCTCCC	1684
2735	QY	TGGTGTGTGCGGGGCTACGACAGCGTGGCTATGGCACCTTTGGTGGAG	2794
1685	DB	TGGTGTGTGCGGGGCTACGACAGCGTGGCTATGGCACCTTTGGTGGAG	1744
2795	QY	ATGCAGGGGCACTGTGGGGCAGGGGCCCATGTGSGCCAGGATAGCTGGGCTGTCTCCC	2854
1745	DB	ATGCAGGGGCACTGTGGGGCAGGGGCCCATGTGSGCCAGGATAGCTGGGCTGTCTCCC	1804
2855	QY	AGTCGAGGAGGAGCAGAGGAGGCGCAGGCTGAGTCCAGTCCGAGGAGCAGCAGG	2914
1805	DB	AGTCGAGGAGGAGCAGAGGAGGCGCAGGCTGAGTCCAGTCCGAGGAGCAGCAGG	1864
2915	QY	AGGCCAGGGCTGAGAGCCCACTTGCCCCAGGTGACGTGCAAGGCCCTGTGCTGAGGTCGGCA	2974
1865	DB	AGGCCAGGGCTGAGAGCCCACTTGCCCCAGGTGACGTGCAAGGCCCTGTGCTGAGGTCGGCA	1924
2975	QY	GGCTCCCCACAGAGCTCTCCAGAGCCCAACCCATCGGAGGACATCGGCGAGCTCTCCC	3034
1925	DB	GGCTCCCCACAGAGCTCTCCAGAGCCCAACCCATCGGAGGACATCGGCGAGCTCTCCC	1984
3035	QY	TGTTGAGATTCGGGACCTGTCCAGGTGATGCGGAGGCGCGGACACAAATATCCTTGGAACA	3094
1985	DB	TGTTGAGATTCGGGACCTGTCCAGGTGATGCGGAGGCGCGGACACAAATATCCTTGGAACA	2044
3095	QY	TTTCCGAGGTGACCCCGCTACCTCAACCTCTCAGACCTGTACGATATCAAGTACCTCC	3154
2045	DB	TTTCCGAGGTGACCCCGCTACCTCAACCTCTCAGACCTGTACGATATCAAGTACCTCC	2104
3155	QY	CATTTCAGTTATGATCTTCAGGAAGTCCCAAGTCCGCTCAGCCAGGCGCCCTCCC	3214
2105	DB	CATTTCAGTTATGATCTTCAGGAAGTCCCAAGTCCGCTCAGCCAGGCGCCCTCCC	2164
3215	QY	CCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCAAGTGGCCCTCGCCAGGTGAAAC	3274
2165	DB	CCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCAAGTGGCCCTCGCCAGGTGAAAC	2224
3275	QY	TGGGCCCCCACGACGGCTTGAGATCAACAGAGGAGTCAGAGGATGTGGACGGGCTGCTGG	3334

RESULT 11
ABN79527
ID ABN79527 standard; cDNA; 382 BP.
XX
AC ABN79527;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human kinase-like ORF4474 cDNA, SEQ ID NO:8947.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibitor; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190366-A2.
XX
PD 29-NOV-2001.
XX
XX
PF 24-MAY-2001; 2001WO-US017076.
XX
PR 24-MAY-2000; 2000US-0206690P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Leach MD, Shimkets RA;
XX
XX WPI; 2002-106200/14.
DR
DR P-PSDB; ABP35501.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.
XX
PS Claim 1; Page 2478; 2508pp; English.
XX
XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79527 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antinfertive activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester

CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases
XX
SQ Sequence 382 BP; 86 A; 104 C; 126 G; 65 T; 0 U; 1 Other;
Query Match 6.9%; Score 358.4; DB 6; Length 382;
Best Local Similarity 99.7%; Pred. No. 1.4e-55;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 502 GGTGGCCAGTGTCTGCAAGGACAGAGCTGCTGGTGGTGGGGGGCAATGAGCCGAC 561
DB 13 GGTGGCCAGTGTCTGCAAGGACAGAGCTGCTGGTGGTGGGGGGCAATGAGCCGAC 72
QY 562 TCAGAGAGCAAGGACCGGAGGAGCTGCTCTCTATGAGGTCAAGGAGAGATT 521
DB 73 TCAAGAGCAAGGACCGGAGGAGCTGCTCTCTATGAGGTCAAGGAGAGATT 132
QY 622 GGAAGGGGGGTGTTGGCTTCTGTAAGAGAGTGACGACCAAGAGAAACAAGATCTTTGTC 691
DB 133 GGAAGGGGGGTGTTGGCTTCTGTAAGAGAGTGACGACCAAGAGAAACAAGATCTTTGTC 192
QY 682 GCTGCCAAGTTTATCCCTACGAGAGCAAGTCCGGGCCAGGCATACAGGAGCGAC 741
DB 193 GCTGCCAAGTTTATCCCTACGAGAGCAAGTCCGGGCCAGGCATACAGGAGCGAC 252
QY 742 ATCTTGGCGCGCTGAGCCACCCGCTGCTCAGCGGGCTGCTGGACCACTTTGAGACCCGC 801
DB 253 ATCTTGGCGCGCTGAGCCACCCGCTGCTCAGCGGGCTGCTGGACCACTTTGAGACCCGC 312
QY 802 AGACCCCTATCTCTATCTGAGAGCTGCTCTATCTGAGAGAGCTGCTGGACCGCTGTAC 861
DB 313 AGACCCCTATCTCTATCTGAGAGCTGCTCTATCTGAGAGAGCTGCTGGACCGCTGTAC 372
RESULT 12
AAF44662
ID AAF44662 standard; cDNA; 7710 BP.
XX
XX AAF44662;
AC
XX
XX 27-MAR-2001 (first entry)
XX
XX Novel protein kinase cDNA, SEQ ID NO: 42.
XX
XX Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
XX immunosuppressive; cardiant; renal; antiinflammatory; antiaethmatic;
XX dermatological; antidiabetic; antinfertility; gene therapy; vaccine;
XX immune disorder; cardiovascular disease; neurodegenerative disease;
XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200073469-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 26-MAY-2000; 2000WO-US014842.
PP
XX
XX 28-MAY-1999; 99US-0136503P.
PR
XX
XX (SUGE-) SUGEN INC.
PA
XX
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
PI
XX

DR WPI; 2001-032161/04.
XX P-PSDB; AAB65635.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
XX treating immune-related diseases and disorders, cardiovascular disease,
XX neurodegenerative diseases and/or cancers.

PS Example 1; Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
XX and the protein kinases they encode may be used in the treatment and
XX diagnosis of diseases associated with inappropriate kinase expression
XX such as immune-related diseases and disorders, cardiovascular disease,
XX neurodegenerative diseases and/or cancers. The nucleic acids and
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays. The kinase polypeptides may be used as antigens in the production
XX of antibodies of kinase expression and activity. Anti-kinase antibodies
XX and kinase antagonists may also be used to down regulate kinase
XX expression and activity. Diseases related to kinase expression and
XX activity include rheumatoid arthritis, atherosclerosis, autoimmune
XX disorders, complications of organ transplantation, myocardial infarction,
XX immune related disorders, cardiomyopathies, strokes, renal failure, oxidative-
XX stress related disorders, chronic inflammatory bowel disease, chronic
XX inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
XX psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
XX disorders

SQ Sequence 7710 BP; 1446 A; 2534 C; 2447 G; 1283 T; 0 U; 0 Other;

Query Match 6.3%; Score 327.6; DB 4; Length 7710;
Best Local Similarity 56.6%; Pred. No. 8.5e-50;
Matches 725; Conservative 0; Mismatches 519; Indels 36; Gaps 5;

QY 256 CTCACGGGCCCCATCGATGAGTAAACATCGAGGATGTCGAGCAGCAGCGCGGA 315
DB 1498 CTGGCAGAGGCCCCCTCGGTTGAGTCCATCATCGAGGAGCTGGAGTGGGGCTGGGAA 1557
QY 316 ACGCCCAATTCGAGGCTATCATTTAGGGGCGACCCACAGCCCTCGGTGACCTGGTACAAAG 375
DB 1558 ACTGCTCGCTTTCGGTGGTTCGAGGGAAACCACTGCCGACATCATGTGGTACAAAG 1617
QY 376 GACAGCTCCAGCTGTGACAGCAGCCGCTTAGCCAGCAGCAGAGGACCAATAC 435
DB 1618 GACAGGTCGCTGACGAGAGCAGCATGTGAGCTTCTGTACGAGGAGATGAGTGC 1677
QY 436 TCCCTGTGCTGAGGCATGTGGCTCGAAGGATGCCGGGTTTACACCTGCTGCCCAA 495
DB 1678 TCCCTGTGCTGCTCAGCAGCGGGGCCAGATGAGGAGGCTTACACCTGCACGCCCCAG 1737
QY 496 AACACTGTGTCAGGCTGCTCTGACGAGGAGCTGCTGTGC -----TT 540
DB 1738 AACCTGGCGGTGAGGCTCTCTGAAAGCAGAGTTGGCTGTGATTCAGCTCAGACAGCT 1797
QY 541 GGGGGGACAAATGAGCCGGAATCAGAGAAACCAAGCCAGGAGGAGCTGCATCTTC 600
DB 1798 ATGAGGTCGAGGGGGTGGGGAGGATGAGGACCATCGAGGAGGAGCTCAGCGACTTT 1857
QY 601 TATGAGGTCAAGGAGGAGATTTGAAGGGGCTGTTTGGCTTCGTAAGAGTGCAGCAC 660
DB 1858 TATGATCCACAGGAGATCGCAGGGGTCTTCTCTACTTGGCGGCACTAGTGAG 1917
QY 661 AAAGAAACAAGATCTTTGGCTGTGCAAGTTCAATCCCTCAGGAGGAGAACTCGGGCC 720
DB 1918 CTAAGCTCCGGCTGGAGTTTGGGGCAAGTTTATCCCGAGCAGCCCAAGCA 1977
QY 721 CAGGCATACAGGAGCAGAGATCCTGGCGGCTGAGCCACCCGCTGTGTACGGGGCTG 780
DB 1978 TCAGGCGTGGGAGGGCGGCTGCTGGCCAGGCTCCAGCAGACTGTGCTCTACTTC 2037
QY 761 CTGAGCCAGTTTGAAGCCGAGAGACCCCTCATCTCTCATCTCTGGAGTGTGCTCATCCGAG 840
DB 2038 CATGAGGCTTCGAGAGGCGCGGGGACTGGTCAATTTGTCACCGAGCTGTCACA---GAG 2094

QY 841 GAGCTGCTGACCGCTGTGTACGAGGAGGCGTGTGTGACGAGGAGCGGAGGTTCAAGGTTCTAC 900
DB 2095 GAGCTGCTGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCTAT 2154
QY 901 ATCCAGCAGCTGTGTGAGGAGGCTGCACTACTGTGACAGCCATGCGGTTCTCCACCTGAC 960
DB 2155 ATGCGGCAAGGTGTAGAGGGAATACACTACTGTGACAGCCAGCCAGTGTGTCACCTCGAT 2214
QY 961 ATAAAGCCCTTAACATCTCTGATGTGTGATCTCTCCCGGGAAGACATTAATA-----ATC 1014
DB 2215 GTCAAGCCCTGAGAACCTGCTGTGTGGGATGCTGTCTCGGCGGAGCAGCAGGTGCGGATC 2274
QY 1015 TCGGCTTTGGCTTTGGCCAGAACATCACCCACAGCAGCTGCGAGTTTCAGCCAGTACGGC 1074
DB 2275 TGTGACTTTGGGAATGCCAGGAGCTGACTCCAGAGAGCCCACTACTGCTGAGTATGGC 2334
QY 1075 TCCCTGAGTTCGTTCTCCCGAGATATCCAGCAGAACCTGTGAGGAGAGCCCTCCGAC 1134
DB 2335 ACACCTGAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCGCTGTCTGGAGTCACTGAC 2394
QY 1135 ATTGGGCGCATGGGTGTCTCTTCTTACCTCAGCTGACCTGCTCATCCCATTTGCCGGC 1194
DB 2395 ATCTGGCTGTGGGTGTGTGGCTTCTCTGTCTGACAGGAATCTCCCGTTTGTGGG 2454
QY 1195 GAGAGTACCGTGGCCACCTCTCTGAAAGCTCTGTGAGGGGCGGCTGTGATGAGCAGCCCC 1254
DB 2455 GAAATGACCGGACCAACATTTGATGAACATCCGAAACTACAACCTGGCTTCGAGGAGACC 2514
QY 1255 ATGGCTGCCACCTCAGCGAAGAGCCGCAAGACTTTCATCAAGGCTACGCTGCAGAGAGCC 1314
DB 2515 ACATTCCTGAGCTGTGAGCAGGAGGCGCGGGGCTTCTCATCAAGGTGTGTGTCAGGAC 2574
QY 1315 CTTAGGCGCGGCTAGTGGCGGCGAGTGCCTCTCCACCCCTGCTTCTGAAATCCATG 1374
DB 2575 CGGCTG---AGACCTTACCGCAGAGAGACCTTAGAACATCCTTGGTT-----CAA 2622
QY 1375 CTGCGGAGGAGGCGCCATTTTCATCAACACCAAGCAGCTCAAGTTCTCTCGGCCCGAAGT 1434
DB 2623 ACTCAGGCAAGGGCGCAGAGGTGAGCAGCGATCACCTGAAGCTATTCTCTCCCGCG 2682
QY 1435 CGCTGCGAGCTTCCCTGATGAGCTACAGTCCATCGTGTGATGCGCTCCATCCCTGAG 1494
DB 2683 AGTGGCAGCGCTCCGAGTCAATGCAATGCCACCTGTGTGTGCGCCCATCCCGAG 2742
QY 1495 CTGCTGCGGGGCCACCCGA 1514
DB 2743 CTGCTGCGGGGCCCGCCAGA 2762

RESULT 13
AAD30565 standard; cDNA; 7789 BP.
XX AAD30565;
XX AC
XX DT
XX 21-MAY-2002 (first entry)
XX Human kinase polypeptide (PKIN-18) cDNA.
XX Human; kinase polypeptide; PKIN-18; gene therapy; Addison's disease;
XX leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
XX acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
XX asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
XX cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
XX cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
XX lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
XX drug screening; transgenic animal; antiinflammatory; hepatotropic;
XX hypotensive; anti-HIV; enzyme; ss.
XX Homo sapiens.
XX WO200208399-A2.
XX

PD	31-JAN-2002.
XX	
FF	20-JUL-2001; 2001WO-US023092.
XX	
PR	21-JUL-2000; 2000US-0220038P.
PR	28-JUL-2000; 2000US-0222112P.
PR	04-AUG-2000; 2000US-0222831P.
PR	11-AUG-2000; 2000US-0224729P.
XX	
PPA	(INCYTE) INCYTE GENOMICS INC.
PPA	(THOR/) THORNTON M.
XX	
PFI	Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
PFI	Patterson C, Rankumar J, Gandhi AR, Policky JL, Baughn MR;
PFI	Tribouley CM, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
PFI	Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
PFI	Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
XX	
PPS	WPI; 2002-206083/26.
XX	
PPT	New human kinase polypeptide, useful in diagnosis, prevention and
PPT	treatment of cancer, immune disorder, growth and developmental disorder,
PPT	cardiovascular disorder and lipid disorder.
XX	
PPS	Claim 5; Page 191-193; 196pp; English.
XX	
CC	The present invention relates to an isolated human kinase polypeptide
CC	(PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
CC	useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
CC	lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
CC	disease, AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
CC	disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
CC	bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
CC	cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
CC	infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
CC	Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
CC	drug screening techniques and to analyse the proteome of a tissue or cell
CC	type. PKIN is useful for creating knockin humanised animals or transgenic
CC	animals to model human diseases, in somatic or germline gene therapy, to
CC	generate a transcript image of a tissue or cell type, for detecting
CC	differences in the chromosomal location due to translocation, inversion,
CC	etc., among normal, carrier or affected individuals, and as hybridisation
CC	probes for mapping naturally occurring genomic sequences. PKIN is useful
CC	in southern or northern analyses, dot blot or other membrane-based
CC	technologies, in PCR technologies, in dipstick, pin, microformat enzyme
CC	linked immunosorbent (ELISA)-like assays and in microarrays utilising
CC	fluids or tissues from patients to detect altered PKIN expression. The
CC	present sequence is human PKIN-18 cDNA. Note: This sequence is said to
CC	encode FKIN-18 referred as SEQ ID NO:18 (AAE19160). However this does not
CC	appear to be the case
XX	
SSQ	Sequence 7789 BP; 1469 A; 2558 C; 2470 G; 1292 T; 0 U; 0 Other;
	Query Match 6.3%; Score 327.6; DB 6; Length 7789;
	Best Local Similarity 56.6%; Pred. No. 8.5e-50;
	Matches 725; Conservative 0; Mismatches 519; Indels 36; Gaps 5;
Qy	256 CTCGAGGGCCCCCATCGATGCAGGTACCATTCAGGATGTGAGGCACAGACAGCGGA 315
Db	1560 CTGGCAGAGGCCCTCGGTTTGAGTCCATCATGAGGAGCGTGGAGGTGGGGG 1619
Qy	316 ACGCCCAATTTCGAGGCTATCATTTAGGGGGGACCACAGCCCTCGGTGACCTGGTACAAG 375
Db	1620 ACTGCTCTTGCGGTGGTGTGTCAGGGGAAAACCACTGCGGACATCATGTGTACAAG 1679
Qy	376 GACAGCTTCAGCTGGTGGACAGCACCGGCTTAGCCAGCAGCAAGAAGGCCACCATAC 435
Db	1680 GACGAGGTGCTGTCACGAGCAGCCATGTGAGCTTCTGTACGAGAGATGAGTGC 1739
Qy	436 TCCTGTGTGTGAGGCATGTGGCTCGAAGGATCGCGGCTTTACACTGCTTGGCCCAA 495
Db	1740 TCCTGTGTGTGCTCAGCAGCGGGGGCCAGGATGGAGGCGTCTACACTGCAACCGCCAG 1799

RESULT 14

ADE47675
 ID ADE47675 standard; DNA; 9698 BP.
 XX
 AC ADE47675;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human NOV14c gene SEQ ID NO:37.
 XX
 KW ds; gene; human; cardiac; antiarteriosclerotic; hypotensive;
 KW immunosuppressive; dermatological; anorectic; cytostatic; antidiabetic;
 KW haemostatic; anti-HIV; antiasthmatic; antibacterial; virucide;
 KW neuroprotective; nontropic; antiparkinsonian; antilipemic; gene therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO2003076642-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024459.
 XX
 PR 02-AUG-2001; 2001US-0309501P.
 PR 03-AUG-2001; 2001US-0310291P.
 PR 08-AUG-2001; 2001US-0310951P.
 PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 14-AUG-2001; 2001US-0312203P.
 PR 17-AUG-2001; 2001US-0313156P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315833P.
 PR 31-AUG-2001; 2001US-0316508P.
 PR 21-SEP-2001; 2001US-0323936P.
 PR 03-DEC-2001; 2001US-0338078P.
 PR 05-FEB-2002; 2002US-0354655P.
 PR 05-MAR-2002; 2002US-0361764P.
 PR 19-APR-2002; 2002US-0373825P.
 PR 15-MAY-2002; 2002US-0380971P.
 PR 16-MAY-2002; 2002US-0380980P.
 PR 16-MAY-2002; 2002US-0381039P.
 PR 28-MAY-2002; 2002US-0383761P.
 PR 29-MAY-2002; 2002US-0383887P.
 PR 01-AUG-2002; 2002US-00210130.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
 PI Pena CPA, Shinkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
 PI Boldog FL, Padigaru M, Smithson G, Shenoy SG, Ji W, Gorman L;
 PI Vermet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
 PI Burgess CE, Khrantsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;
 PI Chaudhuri A, Chant JS, Dippio VA, Edinger SR, Eisen A, Gangolli EA;
 PI Giot L, Ooi CE, Rotherberg ME, Spaderna SK, Hjalt T, Liu X;
 PI Taupier RJ, Catterton E;
 XX
 WPI: 2003-779062/73.
 DR P-PSDB; ADE47676.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT arteriosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
 PT or pharmacogenomics.
 XX
 PS Claim 20; SEQ ID NO 37; 562pp; English.
 XX
 CC The invention relates to a novel (NOVX) human polypeptide. A polypeptide
 CC of the invention has cardiac, antiarteriosclerotic, hypotensive,
 CC

CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
 CC haemostatic, anti-HIV, antiasthmatic, antibacterial, virucide,
 CC neuroprotective, nontropic, antiparkinsonian, and antilipemic activity.
 CC A polynucleotide encoding a polypeptide of the invention may have a use
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, the disease selected from a pathology
 CC associated with the polypeptide. These may also be used in diagnosing,
 CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
 CC hemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting
 CC disorders associated with chronic diseases. The nucleic acids are also
 CC used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine, and pharmacogenomics. The polypeptides are also
 CC useful as vaccines. The present sequence encodes a NOVX polypeptide of
 CC the invention.
 XX
 SQ Sequence 9698 BP; 1693 A; 3352 C; 3163 G; 1490 T; 0 U; 0 Other;
 Query Match 6.3%; Score 327.6; DB 9; Length 9698;
 Best Local Similarity 56.6%; Pred. No. 8.7e-50;
 Matches 725; Conservative 0; Mismatches 519; Indels 36; Gaps 5;
 QY 256 CTCCTGAGGCCCCCATCCATGAGGTAACTGAGGATGTGAGGACAGAGAGCGCGA 315
 DB 4324 CTGGCAGAGGCCCTCGGTTTGAATCATCATGAGGACCTGGAGGTGGGGG 4383
 QY 316 AGGGCCCAATTCGAGGCTATCATTTAGGGGCGACCCACAGCCCTCGGTGACTGTGTAAG 375
 DB 4384 ACTGCTCGTTTGGTGGTGGTGGTGGGAAACCACTGCGGACATCATGTGTACAAG 4443
 QY 376 GACAGGTCAGCTGGTGGACAGCAGCAGCGGTAGCCAGCAGAGAGGACCAACATAC 435
 DB 4444 GACGAGGTGCTGCTACCGAGAGAGCCATGTGAGTTCGTGTACGAGGAGATGATGC 4503
 QY 436 TCCTGCTGCTGAGGATGTGCTCGAAGATGTCGGCGCTTTACACCTGCTGGGCCAA 495
 DB 4504 TCCCTGGTGGTCTCAGCACGGGGGCCAGGATGAGGCGCTTACACCTGCACGCCAG 4563
 QY 496 RACACTGGTGCCAGGTGCTCTGCAAGGCGAGGCTGCTGTGC-----TT 540
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 QY 541 GGGGGGCAATGAGCCGGAATCAGAGAACCAAGCCACCGAGGAGTGTGCACTCTTC 600
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 DB 4744 CGTAGCTCCGGCCTGGAGTTTGGCGGCCAAGTTTCATCCCGAGCCAGCCCAAGGCA 4803
 QY 721 CAGGCATACAGGAGCGAGACATCTCTGGCGGCTGAGCCACCGCTGTGTACGGGGCTG 780
 DB 4804 TCAGCGCTCGGGAGGCCGCTCTGCTGCGCAGGCTCCAGCAGGCTGTCTCTACTTC 4863
 QY 781 CTGGACAGTTTGAGACCCGCAAGACCTCATCTCTGCTGAGGCTGTGCTATCCGAG 840
 DB 4864 CATGAGGCTTCGAGAGCGCGCGGGACTGTGTCATGTACCGAGCTCTGCACA---GAG 4920
 QY 841 GAGCTGTGAGCCGCTGTACAGGAAGGGGCTGTGACGAGGCCGAGGTCAAGTCTAC 900
 DB 4921 GAGCTGTGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCTAT 4980
 QY 901 ATCCAGCAGCTGTGGAGGGGCTGCACTACTCCAGAGCCATGGCGCTTCTCCACTGGAC 960
 DB 4981 ATGGGCGAGTGTAGAGGAGATACACTACTGCAACAGAGCCACGTGTGTACCTCGAT 5040

QY 961 ATAAAGCCCTTAACATCCTGATGGTGCATCTCTGCGGGAAGACATTAA-----ATC 1014
Db 5041 GTCAAGCTTGAGAACCTCTGTTGGGATGGTCTCGGGCGAGCAGAGTGGGATC 5100
QY 1015 TCGACTTTGGCTTTGCCAGGAACATCACCCAGAGAGCTGAGTTCAGCCAGTACGCG 1074
Db 5101 TGTGACTTTGGGATGCCAGAGCTGACTCCAGAGAGCCCACTACTGCCAGTATGCG 5160
QY 1075 TCCCTGAGTTGCTCTCCCGAGATCATCAGCAGAACCTGTGAGGAAGCCTCCGAC 1134
Db 5161 ACACCTGAGTTGTAGACCCGAGATTGTCTCATCAGAGCCCGTGTCTGAGTCACTGAC 5220
QY 1135 ATTGGGCGATGGGTTGATCTCTTACCTCAGCTGACCTGCTCATCCCATTTGCCGCG 1194
Db 5221 ATCTGGCTTGGGTTGTTGGCTTCTCTGTCTGACAGGAATCTCCCGTTTGTGGG 5280
QY 1195 GAGAGTGACCGTGCACCTCTCTGAAGCTCTGGAGGGCGCTGTCTATGGAGCAGCCOC 1254
Db 5281 GAAATGACCGGACAACTTGTATGAACTCGAATCGAATCGAATCGAATCGAATCGA 5340
QY 1255 ATGGTGTGCCACTCAGCGAAGAGCCAAAGATTTCTATGAGCTAGCTGAGAGAGCC 1314
Db 5341 ACATTCCTGAGCTGAGCAGGAGGCGCGGGCTTCTCATAAAGTGTGTGTCAGGAC 5400
QY 1315 CTTAGGCGCGGCTTGTGGCGGCGAGTGTCTCTCCACCCCTGTTCTGAAATCCCATG 1374
Db 5401 CGGCTG---AGACTTACCGGAGAGAGACCTAGAACATCTCTTGGT-----CAAA 5448
QY 1375 CTGCGGAGGGCCACTTCTATACACCAAGCTCAAGTCTCTCTGCGCGGAGT 1434
Db 5449 ACTAGGCGAAGGGCGGAGAGTGAACGGATCCTGAGCTATCTCTCCCGCGG 5508
QY 1435 CGCTGGAGCGTTCCTGATGAGTAAAGTTCATCTGTTGATGCGTCTCATCTCTGAG 1494
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QY 1495 CTGCTGCGGGGCCACCGA 1514
Db 5569 CTGCTGCGGGGCCCGCCAGA 5588

RESULT 15
ADB79958
ID ADB79958 standard; cDNA; 9807 BP.
XX
AC ADB79958;
DT 04-DEC-2003 (first entry)
XX
DE Human kinase protein encoding cDNA SEQ ID NO:1.
XX
KW human; kinase; enzyme; chromosome 2; cytostatic; gene therapy;
KW brain anaplastic oligodendroglioma; lung carcinoma;
KW soft tissue leiomyosarcoma; ovary tumour; germ cell tumour; gene; ss.
XX
OS Homo sapiens.
XX
FH Key
FT 1..9807
FT /tag= a
FT /product= "kinase protein"
XX
PN WO2003076577-A2.
XX
PD 18-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-US006666.
XX
PR 05-MAR-2002; 2002US-0361339P.
XX
PA (APPL-) APPLERA CORP.
XX

PI Yan C, Gan W;
XX
DR WPI; 2003-722329/68.
DR P-PSDB; ADB79958.
XX
PT New peptides related to kinase protein subfamily useful for treating
PT disorders associated with abnormal expression of kinase protein in
PT testis, nervous tissue, fetal, lung, ovary tumor tissue.
XX
PS Claim 4; Fig 1A-C; 86pp; English.
XX
CC The present sequence encodes a human kinase protein (I), which is located
CC to chromosome 2. The present invention also describes an allelic variant
CC or orthologue of (I). (I) has cytostatic activity, and can be used in
CC gene therapy. (I) can be used in substantial and specific assays related
CC to functional information of the protein sequence, to raise antibodies or
CC to elicit immune responses, as reagents in assays to determine the levels
CC of protein in biological fluids. (I) can be used in drug screening assays
CC for identifying agents that are useful in treating disorders associated
CC with the absence of, inappropriate, or unwanted expression of kinase
CC protein in testis, nervous tissue, foetal, lung, brain anaplastic
CC oligodendroglioma, lung carcinoma tissue, soft tissue leiomyosarcoma,
CC ovary tumour tissue, or germ cell tumour tissue. The protein and nucleic
CC acid sequences of (I) are useful as models for the development of human
CC therapeutic targets, in the identification of therapeutic proteins and as
CC targets for the development of human therapeutic agents that modulate
CC protease activity in cells and tissues that express the kinase peptide.
XX
SQ Sequence 9807 BP; 1721 A; 3370 C; 3208 G; 1508 T; 0 U; 0 Other;
Query Match 6.3%; Score 327.6; DB 9; Length 9807;
Best Local Similarity 56.6%; Pred. No. 8.8e-50;
Matches 725; Conservative 0; Mismatches 519; Indels 36; Gaps 5;
QY 256 CTCACAGGCGCCCATCCATCAGGTAAACCATCAGGATGTGAGGACAGAGCGGGA 315
Db 4441 CTGGCAGAGCGCCCTCGCGTTTGTAGTCCATCATGAGGACGTGGAGTGGGGAA 4500
QY 316 ACGGCCCAATTCAGGCTATCATTTAGGGGACCCACAGCCCTCGGTGACCTGATCAAG 375
Db 4501 ATGCTCGCTTTCGGTGTGTGAGGAAACCACTGCGGACATCATGTGTGACAG 4560
QY 376 GACAGCTTCAGCTGGTGGACAGCACCGGGCTTAGCCAGCAGCAAGAGCACCACATAC 435
Db 4561 GACGAGTGTCTGCTACCGCAGAGCAGCCATGTGAGCTTCGTGTACGAGGAAATGAGTGC 4620
QY 436 TCCCTGGTGTGAGGCTATGTGGCTTCGAAGGATCCCGGCGTTTACACCTGCGTGGCCAA 495
Db 4621 TCCCTGGTGTGCTCAGCACCGGGGCCAGGATGGAGGCTCTACACCTGACCGCCAG 4680
QY 496 AACACTGTGGCCAGTGTCTGTCAAGCAGAGCTGCTGTGTC-----TT 540
Db 4681 AACCTGGCGGGTGAAGTCTCTGCAAGCAGAGTGGCTGTGATTCAGCTCAGACAGCT 4740
QY 541 GGGGGGGAACAATGAGCCGGAATCAGAGAAGCAAGCCACCGGAGGAGCTGCATCTCTTC 600
Db 4741 ATGGAGGTCTGAGGGGCTCGGGAGGATGAGGACCATCGAGGAAGAGACTCAGCGACTTT 4800
QY 601 TATGAGTTCAGAGGAGATTTGAAGGGGGTGTGTTGGCTTCGTAAAGAGTGCAGCAC 660
Db 4801 TATGACATCCACAGGATCGGAGGGGTCTTTCTCTACTTGGCGGCATAGTGGAG 4860
QY 661 AAAGGAAACAAGATCTTGTGGCTGCCAAGTTCACTCCCTCTAGCAGCAGAACTCGGGCC 720
Db 4861 CGTAGCTCCGGCTGGAGTTTGGCGGCCCAAGTTTCATCCAGCCAGCCCAAGCAAGCA 4920
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Db 4921 TCAGCGCTCGGGAGGCGCGGCTCTGCGCAGGCTCCAGCAGCTGTGTCTCTACTTC 4980
QY 781 CTGGACCAAGTTTGAAGCCCGCAAGACCTCATCTCTATCTGAGCTGTGCTATCCGAG 840
Db 4981 CATGAGGCTTCGAGAGCGCGCGGGAAGTGTATTGTCTACCGAGCTCTGCACA---GAG 5037

QY 841 GAGCTGCTGACCGCTGTACAGGAAGGGCGTGTGACGGAGGCGAGGTCAAGGTCTAC 900
 Db |||||
 5038 GAGCTGCTGAGGGAATCCCGAGGAACCCACCGTGTGTGAGTCTGAGATCCGGGCTAT 5097
 QY 901 ATCCAGAGCTGTGAGGGGTGACACTACCTGTGACAGCCATGGGTTCTCCACTGGAC 960
 Db |||||
 5098 ATCCGCGAGGTGTAGAGGAATACACTACCTGTGACAGCCAGCGTGTGACCTCGAT 5157
 QY 961 ATAAAGCCCTCTAAACATCTGTATGGTGCATCTGTCCCGGAAGACATTAAA-----ATC 1014
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 5158 GTCAAGCCTGAGAACCTGTGTGGTGTGGTGTGGGCGAGCAGCAGGTGCGGATC 5217
 QY 1015 TGGGACTTTGGCTTTGCCAGAACATCACCCAGAGAGCTGCGAGTTGAGCCATGACGGC 1074
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 5458 ACATTCTGAGCCTGAGCAGGGAGGCGCCCGGGCTTCTCTCATCAAAGTGTGTGGTGGAGAC 5517
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 Db |||||
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 QY 1375 CCTGCGAGAGAGGCCACTTCATCAACACAGCAGCTCAAGTTCTCTGCGCGGAGT 1434
 Db |||||
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 QY 1495 CTGCTGCGGGGCGCCCGGA 1514
 Db |||||
 5686 CTGCTGCGGGCCCCCGAGA 5705

Search completed: April 26, 2004, 09:08:04
 Job time : 1258 secs

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 08:13:13 ; Search time 8097 Seconds
(without alignments)
19203.702 Million cell updates/sec

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Perfect score: 5207
Sequence: 1 cagcagagaaactctctt.....aaaaaaaaaaaaaaaaaaaaa 5207

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: em_estba.*
- 2: em_esthm.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hci.*
- 9: gb_estl.*
- 10: gb_est2.*
- 11: gb_hci.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_lam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_pbg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	848.4	16.3	931	13	BX409793
3	777.4	14.9	924	13	BX409792
4	713.4	13.7	715	12	BM985339

5	666.8	12.8	731	12	BG818748
6	655.6	12.6	683	10	AM862431
7	626.2	12.0	989	13	EX435097
8	554.1	10.4	622	12	BG99843
9	478.4	9.2	480	13	EX280322
10	475	9.1	475	12	BI916955
11	471	9.0	653	13	BF134040
12	463.2	8.9	768	12	BI916956
13	453	8.7	477	12	BG989614
14	434	8.3	517	12	BG989614
15	415.2	8.0	556	12	BI776197
16	398.2	7.6	640	14	CD774776
17	386.8	7.4	526	13	QO554403
18	377.4	7.2	622	14	CF176441
19	340.8	6.5	567	12	BI345924
20	331	6.4	479	10	BF651426
21	324.4	6.2	494	14	CF177813
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23	311.4	6.0	493	10	BE110731
24	307.8	5.9	447	10	BB848582
25	307	5.9	920	10	BF160452
26	303.2	5.8	429	9	A1604658
27	296.6	5.7	494	14	CB713368
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30	274	5.3	427	9	A1006121
31	272.2	5.2	389	13	BY088395
32	267.2	5.1	311	10	BF855491
33	257.4	4.9	570	12	BI345921
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36	246	4.7	397	12	BG986727
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38	238.2	4.6	408	10	BF414891
39	237	4.6	3241	11	AK035543
40	235.2	4.5	418	13	EX636992
41	231.6	4.4	445	13	BY588786
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43	229.4	4.4	368	10	AM425352
44	229.2	4.4	411	12	BI186010
45	209.8	4.0	417	13	BY437537

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

983 bp mRNA linear EST 22-MAY-2003
BX460671 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF017YK06 5-PRIME, mRNA sequence.
BX460671
BX460671.1 GI:31023260
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 983)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1025.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSODF017BF03Q1&cluster=1025.r. Contact :
Peng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF017BF03QP1.

FEATURES

Source

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1. 983
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/clone="CS0DF017YK06"
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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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ORIGIN

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Query Match 17.0%; Score 883.8; DB 13; Length 983;
Best Local Similarity 99.0%; Pred. No. 5.9e-114;
Matches 918; Conservative 2; Mismatches 4; Indels 3; Gaps 3;

QY 2596 GTGGGCTCTCCAGGTGGGACAGAGCTGGCCCTCCCTGATGCGAGGCTGGACC 2655
DB 56 GGGATCTCTCCAGGTGGGACAGAGCTGGCCCTCCCTGATGCGAGGCTGGACC 115
QY 2656 CAGGAGGCTGAGGATCTGCGACCTCCACACCCACCTTGACAGCGGCTCAGGAACAGGTG 2715
DB 116 CAGGAGGCTGAGGATCTGCGACCTCCACACCCACCTTGACAGCGGCTCAGGAACAGGTG 175
QY 2716 ACATGCGCAAGTTCTCTGCTGGTGTGCGGGGGCTACGAGCGCTGCTGCTATGGC 2775
DB 176 ACATGCGCAAGTTCTCTGCTGGTGTGCGGGGGCTACGAGCGCTGCTGCTATGGC 235
QY 2776 ACCTTTGCTTTGTTGGAGATGTCAGGGGGCATGCTGGGGCAGAGGGGCCCATGTGGGCCAGG 2835
DB 236 ACCTTTGCTTTGTTGGAGATGTCAGGGGGCATGCTGGGGCAGAGGGGCCCATGTGGGCCAGG 295
QY 2836 ATAGCTGGGCTGCTCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2895
DB 296 ATAGCTGGGCTGCTCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355
QY 2896 CAGTCGAGGAGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2955
DB 356 CAGTCGAGGAGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 2956 CCTGTGCTGAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3015
DB 416 CCTGTGCTGAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 475
QY 3016 GACATCGGCGAGGTCCTCTGCTGAGATCCGGGACCTGTGAGGTGATGCGGAGGCGGCC 3075
DB 476 GACATCGGCGAGGTCCTCTGCTGAGATCCGGGACCTGTGAGGTGATGCGGAGGCGGCC 535
QY 3076 GACACATATCCCTGGAATTCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3135
DB 536 GACACATATCCCTGGAATTCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595
QY 3136 TAGCATATCAAGTACTCCCATTCGAGTTTATGATCTCAGAAAGTCCCAAGTCGGCT 3195
DB 596 TAGCATATCAAGTACTCCCATTCGAGTTTATGATCTCAGAAAGTCCCAAGTCGGCT 655
QY 3196 CAGCCAGAGCCGCTCCCTCCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3255
DB 656 CAGCCAGAGCCGCTCCCTCCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715
QY 3256 TGGCCCTGCGCAGGTGAATGTCGGCCCCCAGCAGGCTT-GGAGATCAAGAGGAGTCA 3314
DB 716 TGGCCCTGCGCAGGTGAATGTCGGCCCCCAGCAGGCTTGGAGATCAAGAGGAGTCA 775
QY 3315 GGATGTGGAGCGGCTGCTGGCAGAGGCTGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3374
DB 776 GGATGTGGAGCGGCTGCTGGCAGAGGCTGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 835
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QY 3375 GTACAGCAGGCTCTTCCACATCTCC-TGGGAGGACCTGGCGCTGGATGAGCCTGCAGAGC 3433
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QY 3434 T-GGGGCTGGGTGAGAGAGTGAAGGCTCCGTGGAGCAGATCTCCCGGATCTCTGAGGCG 3492
DB 896 TGGGGGCTGGGTGAGAGAGTGAAGGCTCCGTGGAGCAGATCTCCCGGATCTCTGAGGCG 955
QY 3493 AGGCCGGAAGGCTCTGGAGAAAGGAGGGG 3519
DB 956 AGGCCGGAAGGCTCTGGAGAAAGGAGGGG 982

RESULT 2
BX409793 931 bp mRNA linear EST 13-MAY-2003
LOCUS BX409793
DEFINITION BX409793 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF017YK06 5-PRIME, mRNA sequence.
ACCESSION BX409793
VERSION BX409793.1 GI:30640364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1025.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF014ZC08_AF01308_2&cluster=1025.r.
Contact: Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF014ZC08_AF01308_2.
Location/Qualifiers
1. 931
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/tissue_type="FETAL BRAIN"
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
```

ORIGIN

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Query Match 16.3%; Score 848.4; DB 13; Length 931;
Best Local Similarity 95.9%; Pred. No. 5.3e-109;
Matches 896; Conservative 0; Mismatches 33; Indels 5; Gaps 3;

QY 3410 TGGCGCTGGATGAGCTGCGAGAGCTGGGGCTGCTGAGAGAGTGAAGGCTCCGTGGAGC 3469
DB 2 TGGCGCTGGCGAAGCTGCGAGAGCTGGGGCTGCTGAGAGAGTGAAGGCTCCGTGGAGC 61
QY 3470 ACATCTCCCGATCCTGAAGGCGAGGCGCGGAAGGCTTGAGAGAGGAGGCGCCCCCAGGA 3529
DB 62 ACATCTCCCGATCCTGA--GGGCGAGCGCGGAGGCTTGAGAGAGGAGGCGCCCCCAGGA 119
QY 3530 AGAAGCAGGCGCTTGTCTTCTCGGCTCTCAGGTCTGAAGAGCTGGGAGCGGAGCGCCGA 3589
DB 120 AGAAGCAGGCGCTTGTCTTCTCGGCTCTCAGGTCTGAAGAGCTGGGAGCGGAGCGCCGA 179
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QY	3590	CATTCTTAAGGAGCTCTCAGATGAGACTGTGGTCTCTGGGCCAGTCAGTACACTGGCCT	3649
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QY	3650	GCCAGGTGTACGCCAGCCAGCTGCCAGGCCACCTGGAGCAAGACGGAGGCCCCCTGG	3709
Db	240	GCCAGGTGTACGCCAGCCAGCTGCCAGGCCACCTGGAGCAAGACGGAGGCCCCCTGG	299
QY	3710	AGAGCAGCAGCCGTGTCTCATCTCTGCGCACCTCTCAAGAACTTTCAGCTTCTGACCATCC	3769
Db	300	AGAGCAGCAGCCGTGTCTCATCTCTGCGCACCTCTCAAGAACTTTCAGCTTCTGACCATCC	359
QY	3770	TGGTGGTGTGGCTCAGGACCTGGGTGTGTACACCTTGACGCTGAGCAATGCGCTGGGGA	3829
Db	360	TGGTGGTGTGGCTCAGGACCTGGGTGTGTACACCTTGACGCTGAGCAATGCGCTGGGGA	419
QY	3830	CAGTGAACACACAGCGGCGTCTCCGGAAGGACAGAGCGCCCTCATCTTGGCCATGCCCGG	3889
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QY	3950	GCCCTGTGACCTACATTTGTGCAGTGCAGCTAGAAAGCGGCGAGCTGGACCACTTGGCCT	4009
Db	540	GCCCTGTGACCTACATTTGTGCAGTGCAGCTAGAAAGCGGCGAGCTGGACCACTTGGCCT	599
QY	4010	CCGACATCTTTGACTGTCTTACCTGACACAGCAAGCTCTCCGGGAGTGGCACTTACACT	4069
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QY	4070	TCCGACACGGCATGTGTACGAAAGCAGAAATGGTCCCTTACAGCAGCCCTTCGAGACAAG	4129
Db	660	TCCGACACGGCATGTGTACGAAAGCAGAAATGGTCCCTTACAGCAGCCCTTCGAGACAAG	719
QY	4130	TCCTCTCTGGAGGGCCAGCCACCTGGCTCTGAGAGGAGAGCCAGGGGGCGGTACGCC	4189
Db	720	TCCTCTCTGGAGGGCCAGCCACCTGGCTCTGAGAGGAGAGCCAGGGGGCGGTACGCC	779
QY	4190	AAACCCCTGCCGACACAAAGACTTTCGATTCGAGACACAGATCCAGAGGGGCGCTTCA	4249
Db	780	AAACCCCTGCCGACACAAAGACTTTCGATTCGAGACACAGATCCAGAGGGGCGCTTCA	839
QY	4250	GCGTGGTGGCGCAATGTGGGGAAGGCCACAGCGGGCGGCGCTGGCGCCCAAGATCATCC	4309
Db	840	GCGTGGTGGCGCAATGTGGGGAAGGCCCAAGCGGCGGCGCTGGCGCC--AGNACATCC	898
QY	4310	CCTACCACCCCAAGACAAGACAGCTGTCTGCG	4343
Db	899	CCTACCACCCCA--GGACAGNCAAGACAGTGTCTGCG	930

[illegible]

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1025.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0AF014ZC08.AF01308.1&cluster=1025.r>. Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAF014ZC08.AF01308.1.

Location/Qualifiers

1..924

organism="Homo sapiens"

molecule_type="mRNA"

db_xref="taxon:9606"

clone="CS0DF017YK06"

tissue_type="FETAL BRAIN"

dev stage="fetal"

clone lib="Homo sapiens FETAL BRAIN"

note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

FEATURES

source

ORIGIN

Query Match	14.9%	Score 777.4	DB 13	Length 924
Best Local Similarity	96.4%	Pred. No. 4.6e-99		
Matches 848	Conservative 0	Mismatches 24	Indels 8	Gaps 5
QY	3421	GAGCCTGACAGCTGGGGCTGCGTGAGAGAGTGAAGAGCTCGTGGAGCACATCTCCCGG	3480	
DB	1	GAGCCTGACAGAGCTGGGGCTGCGTGAGAGAGTGAAGAGCTCGTGGAGCACATCTCCCGG	60	
QY	3481	ATCTGTGAAGGCGAGGCGGAGAGTCTGGAGAGAGAGGGGCCCCCAGAGAGAGACCGAGC	3540	
DB	61	ATCTGTGAAGGCGAGGCGGAGAGTCTGGAGAGAGAGAGGGGCCCCCAGAGAGAGACCGAGC	120	
QY	3541	CTTGTCTTCCTTCGGCTCTCAGGTCTGAAGAGCTGGGACCGAGCGCCGACATTCCTAAGG	3600	
DB	121	CTTGTCTTCCTTCGGCTCTCAGGTCTGAAGAGCTGGGACCGAGCGCCGACATTCCTAAGG	180	
QY	3601	GAGCTCTCAGATCAGACTGTGTGTCTGGGCCAGTCAGTGAACACTGTGGCTGTCCAGGTGTCA	3660	
DB	181	GAGCTCTCAGATCAGACTGTGTGTCTGGGCCAGTCAGTGAACACTGTGGCTGTCCAGGTGTCA	240	
QY	3661	GCCAGACGACTGCCAGGCGCACTTGGAGCAAGACGAGCGCCCTCTGGAGAGCAGCAGC	3720	
DB	241	GCCAGACGACTGCCAGGCGCACTTGGAGCAAGACGAGCGCCCTCTGGAGAGCAGCAGC	300	
QY	3721	CGTGCTCTCATCTGTGCCACCTCAAGAACTTCCAGCTTCTGACCATCTCGTGGTGGTG	3780	
DB	301	CGTGCTCTCATCTGTGCCACCTCAAGAACTTCCAGCTTCTGACCATCTCGTGGTGGTG	360	
QY	3781	GCTGAGGACCTGGGTGTGTACACTTGCAGCTGAGCAATGGCTGGGGACAGTGAACACC	3840	
DB	361	GCTGAGGACCTGGGTGTGTACACTTGCAGCTGAGCAATGGCTGGGGACAGTGAACACC	420	
QY	3841	ACGGGCTCTTCGGAGAGCAGAGCGCCCTCATCTTCCGCATCCCGGATATCGGGGAG	3900	
DB	421	ACGGGCTCTTCGGAGAGCAGAGCGCCCTCATCTTCCGCATCCCGGATATCGGGGAG	480	
QY	3901	GTTGACCGGATGGGGTGTGTGTCTTGGAGCCGCTGGGAATCCTACGCCCTGTGACC	3960	
DB	481	GTTGACCGGATGGGGTGTGTGTCTTGGAGCCGCTGGGAATCCTACGCCCTGTGACC	540	
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DB	541	TACATTGTGCAGTGCAGCTACGAAGCGGCGAGCTGGACCACTGTGGCTCCGACATCTTT	600	
QY	4021	GACTGTGTCTACTGACCGAGCAAGCTCTCCGGGGTGGCACCTTACACTTCCCGCAGGCA	4080	
DB	601	GACTGTGTCTACTGACCGAGCAAGCTCTCCGGGGTGGCACCTTACACTTCCCGCAGGCA	660	
QY	4081	TGCTGCAGCAAGCAGGAATGGGTCCCTACAGCAGCCCTCGGAGCAAGTCTCTCTGGGA	4140	

540	TTGTGTCGCAATCGCGAAGAGACGCGCGTGTGTATACAGAGGCAACAACCTGGCCCCAG	599
5098	GTGCGCTGAGGGTGCCTCCCGGCCACACCTTGGTCTCCCGCTGGGGGTGCGTGCAGACG	5157
600	GTGCGCTGAGGGTGCCTCCCGGCCACACCTTGGTCTCCCGCTGGGGGTGCGTGCAGACG	659
5158	CGCCCAATAAAAACGCACACGCGCGGCGAGAAAAAAGAAAAAAGAAAAA 5207	
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RESULT 6		
AW862431		
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TITLE		
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MEDLINE		
PUBMED		
COMMENT		
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ORIGIN		
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Best Local Similarity	99.0%	Pred. No. 5.1e-82;
Matches 669;	Conservative	0; Mismatches 6; Indels 1; Gaps 1;
Qy	3753	CCAGCTTTCACCATCTGCTGGTGGTGGCTCGAGGACCTGGGTGTGTACACCTGCAGCGT 3812
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QY 3813 GAGCAATGGCTGGGACAGTGACACACACGGGGCTCTCCGAAGGAGGAGAGCGCCCTC 3872
Db 61 GAGCAATGGCTGGGACAGTGACACACACGGGGCTCTCCGAAGGAGGAGAGCGCCCTC 120
QY 3873 ATCTTGGCCATGCCCGATATGGGAGAGTGACCGGATGGGCTGCTGGTCTGGAA 3932
Db 121 ATCTTGGCCATGCCCGATATAGGGAGAGTGACCGGATGGGCTGCTGGTCTGGAA 180
QY 3933 GCCGTGGAACTCTACGGCCCTGTGACCTTACATTTGTGAGTGACGCTTAGAAGCGGCGAG 3992
Db 181 GCCGTGGAACTCTACGGCCCTGTGACCTTACATTTGTGAGTGACGCTTAGAAGCGGCGAG 240
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QY 4053 GGCTGGCACTACACCTTCCGACGCGCATGTGTACGACGAGGAGGAGGAGGAGGAGGAG 4112
Db 301 GGCTGGCACTACACCTTCCGACGCGCATGTGTACGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 4113 CAGCCCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4172
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QY 4233 CCAGAGGGGGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4292
Db 481 CCAGAGGGGGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 4293 GGGCGGCAAGATATCCCTTACACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4352
Db 541 GGGCGGCAAGATATCCCTTACACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 4353 GGGCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4412
Db 601 GGGCGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 4413 CCGGCACTGGTGGCT 4428
Db 661 CC-GCACTGGTGGCT 675
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LOCUS
DEFINITION BX435097 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION CSODF017YK06 3-PRIME, mRNA sequence.
VERSION BX435097.1 GI:30783342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1025.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF017YK06&cluster=1025.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF017YK06
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FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
ORIGIN
Query Match 12.0%; Score 626.2; DB 13; Length 989;
Best Local Similarity 96.7%; Pred. No. 6.4e-78;
Matches 672; Conservative 0; Mismatches 18; Indels 5; Gaps 3;
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QY 4535 CCCAGTACTCTCACAACCCAGCAC--ATCCTGACACCTGAGACCTGAGGTCCGAGAACATGATC 4593
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QY 4654 GAGAAGGTGTCGCCCTCAGACAGTTCACAGGACTTACCTAGAGACCATGGTCCAGAGCTC 4713
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QY 4714 CTGGAGGGCCAGGGGGCTGTTCACACAGACAGATCTGGGCCATCGGTGTGACAGCCTTC 4773
Db 515 CTGGAGGGCCAGGGGGCTGTTCACACAGACAGATCTGGGCCATCGGTGTGACAGCCTTC 456
QY 4774 ATCATGCTGAGCGCCGAGTATACCGGCTGAGCAGGAGGAGGTGCACGCGACCTGACAGAGA 4833
Db 455 ATCATGCTGAGCGCCGAGTATACCGGCTGAGCAGGAGGAGGTGCACGCGACCTGACAGAGA 396
QY 4834 CTGGCAGAGGGCTGTGTCGGCTGAGCGCTGTAGCGGGGCTGTCGGGGGCGCGCTG 4893
Db 395 CTGGCAGAGGGCTGTGTCGGCTGAGCGCTGTAGCGGGGCTGTCGGGGGCGCGCTG 336
QY 4894 GCCTTCTCTGCGACAGCTCTGTGCGCCAGCTTGGGGCGGGCCCTGTCGCGTCCAGCTGC 4953
Db 335 GCCTTCTCTGCGACAGCTCTGTGCGCCAGCTTGGGGCGGGCCCTGTCGCGTCCAGCTGC 276
QY 4954 CTGAGTGCCTGCTGGCTAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5013
Db 275 CTGAGTGCCTGCTGGCTAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 216
QY 5014 TTCCTTACCGCGGGCTGCGCGTCTTGTGCGCAATCGCGAGAGAGAGCGCGGCTGCTG 5073
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QY 5074 TACAAGAGGACACACCTGCGCCAGGTGCGTGAAGGAGTCCCGCGGCGCACACCTTGGTCT 5133
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EST 13-JUN-2001
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VERSION        BG999843.1  GI:14403915
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SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 622)
AUTHORS      Dias, Nervo, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=WR3&tl2=WR3-HN0063-
              030101-001-h03&tl3=2001-01-03&tl4=1)
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                  /note="Organ: head normal; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the puc 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."

FEATURES             source
  source
    Query Match      10.4%; Score 541; DB 12; Length 622;
    Best Local Similarity 98.8%; Pred. No. 5.6e-66;
    Matches 566; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy 2933  CACTGCCCCAGGTCAGTCAAGGCTGTGCTGAGGTGGGAGGCTCCACCA-GGAGC 2991
Db 622   CACTGCCCCAGTTCA-TCCAGGGCTGTTCTGAGGTGACAGGGCTCCACCGAGGAGC 564

Qy 2992  TCTCCAGAGCCACCCATGGAGGACATCGGGCAGGTCTCCCTGGTCCAGATCGGGAC 3051
Db 563   TCTCCAGAGCCACCCATGGAGGACATCGGGCAGGTCTCCCTGGTCCAGATCGGGAC 504

Qy 3052  CTGTGAGGTGATCGGAGGCGGCCACACATATCCCTGGACATTTCCGAGGTGAGACCC 3111
Db 503   CTGTGAGGTGATCGGAGGCGGCCACACATATCCCTGGACATTTCCGAGGTGAGACCC 444

Qy 3112  GCCTACTCMACTCTCAGACCTGACGATATCAGTACCTCCCACTTCGAGTTTATGATC 3171
Db 443   GCCTACTCMACTCTCAGACCTGACGATATCAGTACCTCCCACTTCGAGTTTATGATC 384

Qy 3172  TTCAGGAAGTCCCCAAGTCCGCTCAGCCAGGCGGCCCTCCCCCATGGCTGAGGAGGAG 3231
Db 383   TTCAGGAAGTCCCCAAGTCCGCTCAGCCAGGCGGCCCTCCCCCATGGCTGAGGAGGAG 324

LOCUS      BX280322      480 bp      mRNA      linear      EST 04-MAR-2003
DEFINITION BX280322 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE998D1910821 ;
IMAGE:4914402, mRNA sequence.
ACCESSION  BX280322
VERSION    BX280322
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
            Radelof, U., Schneider, D. and Korn, B.
TITLE       Human Unigeneset - RZPD3
JOURNAL     Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGE998D1910821.
            RZPDLIB; I.M.A.G.E. cDNA clone collection;
            Human Unigeneset - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/cloneCards/cgi-
            bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13u, Primer sequence: CGTTGTAACAGCGGCCAGT.

FEATURES             Location/Qualifiers
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      Site 2: SmaI; Cloned unidirectionally. Primer: Oligo dT.
      Average insert size 2.3 kb. Constructed by Life
      Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match      9.2%; Score 478.4; DB 13; Length 480;
Best Local Similarity 99.8%; Pred. No. 3.3e-57;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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	QY	CTGAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCACCAGTAGTCCTGCACAACCAAGC	4555
4496	Dd	CCGAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCACCAGTAGTCCTGCACAACCAAGC	60
	QY	ACATCTCTGCACCTTGAGACTCAGGTCGCGAACAATGATCATCACCGAAATCAAACCTGCTCA	4615
4556	Dd	ACATCTCTGCACCTTGAGACTCAGGTCGCGAACAATGATCATCACCGAATCAAACCTGCTCA	120
61	QY	AGGTCTGTGACCTTGGGCGAATTGACAGAGCCTGAGCCAGGAGAGGTGTGCCCTCAGACA	4675
4616	Dd	AGGTCTGTGACCTTGGGCGAATTGACAGAGCCTCAGCCAGGAGAGGTGTGCCCTCAGACA	180
121	QY	AGTTCAAAGGACTACCTAGAGACCATGGCTCCAAGAGCTCTGTGAGGGCCAGAGGGGCTGTC	4735
4676	Dd	AGTTCAAAGGACTACCTAGAGACCATGGCTCCAAGAGCTCTGTGAGGGCCAGAGGGGCTGTC	240
181	QY	CACAGACAGACATCTGGCCATCGGTGTACAGACCTTCATCATGCTGAGCGCCAGTAGCC	4795
4736	Dd	CACAGACAGACATCTGGCCATCGGTGTACAGACCTTCATCATGCTGAGCGCCAGTAGCC	300
241	QY	CGTGTAGCAGCGAGGTTGACGCGACCTCGACAGAGAGACTGCGCAAGGGGCTGTGTCGGC	4855
4796	Dd	CGTGTAGCAGCGAGGTTGACGCGACCTCGACAGAGAGACTGCGCAAGGGGCTGTGTCGGC	360
301	QY	TGAGCCGCTCTAGCGGGGCTGTCCGGGGGCGCGTGGCTTCTCTCGCAGACACTCTGT	4915
4856	Dd	TGAGCCGCTCTAGCGGGGCTGTCCGGGGGCGCGTGGCTTCTCTCGCAGACACTCTGT	4975
361	QY	CGCCCCAGCCCTGGGGCCGCCCTTCGCGCTCCAGTGTCTGCAGTGGCCGTGCTTAACAG	4935
4916	Dd	CGCCCCAGCCCTGGGGCCGCCCTTCGCGCTCCAGTGTCTGCAGTGGCCGTGCTTAACAG	4995

RESULT 10
B1916955
LOCUS
DEFINITION
B1916955 475 bp mRNA linear EST 16-OCT-2001
603177769F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:524025 5',
mRNA sequence.

BI916955
ACCESSION
VERSION
BI916955.1
KEYWORDS
EST.
GI:16180909

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE
I (bases 1 to 4/5)
NTH-MGC http://mgc.nci.nih.gov/

AUTHORS
 NIH-MGC <http://mgc.ncl.nih.gov/>;
 TITLE
 National Institutes of Health; Mammalian Gene Collection (MGC)

JOURNAL
UNPUBLISHED (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I. M. A. G. E. Consortium (ILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11610 Row: 9 Column: 18
High quality sequence span: 475

high quarry sequence stop: 473.

FEATURES

Location/Qualifiers

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1. .475

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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Tissue in slices examined had

and male age 26 weeks. Library is oligo-dT primed and

Age Group	Percentage
18-24	15
25-34	35
35-44	25
45-54	15
55-64	10
65-74	5
75-84	2
85+	1

[REDACTED]

directionally cloned (EcoRV site is destroyed upon c-tong). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics' tracking code 017. Note: this is a NIH MGC Library."

Query Match	9.1%	Score 475;	DB 12;	Length 475;
Best Local Similarity	100.0%;	Pred. No. 9.8e-57;		
Matches 475;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
3637	GTGACACTGGCCCTGCCAGGTGTACGCCACAGCAGCTGCCACAGGCACCTCGAGCAAGAC	3696		
Db	1 GTGACACTGGCCCTGCCAGGTGTACGCCACAGCAGCTGCCACAGGCACCTCGAGCAAGAC	60		
3697	GGAGCCCCCTGGAGAGCAGCAGCGTGTCTCATCTCTGCCACCTTCAGAACTTCCAG	3756		
Db	61 GGAGCCCCCTGGAGAGCAGCAGCGTGTCTCATCTCTGCCACCTTCAGAACTTCCAG	120		
3757	CTTCTGACCACTCTGGTGGTGGCTCAGGACCTGGGTGTGTACACTGCAGCGTGAGC	3816		
Db	121 CTTCTGACCACTCTGGTGGTGGCTCAGGACCTGGGTGTGTACACTGCAGCGTGAGC	180		
3817	AATGCGCTGGGGACAGTGAACCAACGCGGTCTCTCGGAAGGCAGAGCGCCCTCATCT	3876		
Db	181 AATGCGCTGGGGACAGTGAACCAACGCGGTCTCTCGGAAGGCAGAGCGCCCTCATCT	240		
3877	TCGCCATCCCGGATATCGGGCAGGTGTACCGGATGGGGTGTCTGTGTCTCGAAGCCC	3936		
Db	241 TCGCCATCCCGGATATCGGGCAGGTGTACCGGATGGGGTGTCTGTGTCTCGAAGCCC	300		
3937	GTGGAATCTTACGGCCCTGTGACCTTACATTTGTGCAGTGCAGCCTTAGAAGCGCGCAGCTGG	3996		
Db	301 GTGGAATCTTACGGCCCTGTGACCTTACATTTGTGCAGTGCAGCCTTAGAAGCGCGCAGCTGG	360		
3997	ACCACACTGGCCCTTCGACACTTTTGCATCTGCTACTCTGCACCAAGCTCTCTCCCGGGT	4056		
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4057	GGCACTTACACTTTCGGCACCGCATGTGTGACGAAGGCAGGAATGGTCTCCCTACA	4111		
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RESULT 11
BV739930
LOCUS
BV739930 653 bp mRNA linear EST 17-DEC-2002
DEFINITION
BV739930 Riken full-length enriched, pooled tissues, 16 days
embryo, etc. Mus musculus cDNA clone I32006N21 5', mRNA sequence.
ACCESSION
BV739930
VERSION
BV739930.1 GI:27163955
KEYWORDS
Egr.

Isr.	Mus musculus (house mouse)	
SOURCE	Mus musculus	
ORGANISM		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 653)	
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,	

Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schomach, C., Cojoberi, T., Saidarelli, R., Hill, D. P., Bult, C.,
Rume, D. A., Quackenbush, J., Schriml, L. M., Kanepin, A., Matsuda, H.,
Bata, C. S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L. E., Cousins, S., Pallia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Garibaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lennard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, D., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

QY		3430	GAGCTGGGGTGGGTGAGAGAGTGGAAGGCCTCCGTGGAGCACATCTCCCGAATCCTGAAG	3489
Dd		5	GAGCTTGGGCTGGGCCAGAGGGTGAAGGTTTCATATGGTCACTCTCCAGATCCTCAAG	64
QY		3490	GGCAGGCCGAAAGTCTTGAGAGAAGAGGGGGCCCCCAGAGAAGACGAGCCTTGCTTCC	3549
Dd		65	GGCAGGCCGAAGTCTTGAGAGGGAAGGGCTCTCCAGANAAGGAGCGCTTAGCTTCT	124
QY		3550	TTCGGGCTCTCAGGTCGTAGAGACTGGGACCGAGGGCGCATCTCTTAAGGAGCTCTCA	3609
Dd		125	TTCGGGCTGTACGGCTGAAGGGCAGGGACCAAGCACATCTCTCTAAGAGAACTCTCA	184
QY		3610	GATGAGACTGTGTCTTGGGCGCATGTAGTACA CTGGGCTGCCAGTGTGTCAGGCCACGCCA	3669
Dd		185	GACAGAGCTGTGTCTTGGGCGCAATCAGTGCACATGGGCTGCCAGTGTGTTGGGCCACGCCA	244
QY		3670	GCTCCCAGAGCCACCTGGAGCAAAGACGGAGGCCCTTGGAGAGCAGCACCGGTGCTCTC	3729
Dd		245	ACTGCCAGGCTACCTGGAGCAAGAATGGGTCTCTCTGGAGAGCAGCGGCCACCTCCTC	304
QY		3730	ATCTCTGCCACCCTCAAGAACTTCAGTCTTGACACCTCTGGTGGTGGTGGGTGAGGAC	3789
Dd		305	ATTCTCTTCACTTGAGAACTCTCCAGTCTGTGTGACCACTCTGTCTGTGTGAACGACGCT	364

3790	CTGGGTTGTACACCTGTGAGCGCTGTGAGCAATGGCTTGGGGACAGTGCACCAACCGGGCGTGC	3849
365	CTGGGCACATATACCTTGCCTGTGTGAGCAACCCGCTTGGGGACAGCAGTTCACACAGGTGTC	424
3850	CTCCGGAAGGCAGAGCGCCCTCATCTTTCGCGCATGCCCGGATATCGGGGAGGTGTACGGC	3909
425	CTCCGGAAGCAGAGCGCCCTCATCTTCTCCAGCCCTGAGTGGGGAGCACTATACAG	484
3910	GATGGGTGTGTGTGTCTGTGAAGCCCTGTGAATCTTACGCCCTGTGACCTACATTTGTG	3969
485	GATCGGTGTGTGTGTCTGTGAAGCCCTGTGAATCTTGTGCCCGGTGACCTACATTTGTG	544
3970	CAGTGAGCCTAGAAAGCGGCGAGCTGGACACACTGTGCCCTCCGACATCTTTGACTCTCTGC	4029
545	CAGTGTGTATAGAGGAGGAGCTGGACAACCTTGGCTTCAGACATCTCTGACTGCTCTGC	604
4030	TACCTACACGACAGCTCTCCCGGGGTGGCACCTACACCTTCCGCACGG	4078
605	TACCTACTGNCAGCTATCGAGGGGTGGCATGTATATCTTTCGGCAG	653

RESULT 12
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 DEFINITION 601778492F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4006702 5',
 mRNA sequence.
 BF134040
 ACCESSION

accession EPI34040
 version 1
 keywords GI:10973080
 source Mus musculus (house mouse)
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 768)
 reference NIH-WGC <http://mgc.nci.nih.gov/>.
 authors National Institutes of Health, Mammalian Gene Collection (MGC)
 title Unpublished (1999)
 journal Contact: Robert Strausberg, Ph.D.
 comment Email: cgabbs-remail.nih.gov
 tissue procurement: Gilbert Smith, Ph.D.
 cDNA library preparation: Life Technologies, Inc.
 cDNA library arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA sequencing by: Invitrogen, Inc.

www.cdc.gov/nczod/cid/ncezod/
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM9238 row: 9 column: 23
 High quality sequence stop: 736.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4006702"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH108"
/clone_lib="NCI CGAP Lu30"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-1TR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 8.9%; Score 463.2; DB 10; Length 768;
Best Local Similarity 81.0%; Pred. No. 4.2e-55;
Matches 601; Conservative 0; Mismatches 133; Indels 8; Gaps 5;

QY 4105 CCTACAGAGCCCTCGAGAGAGGTCCTTCCTGGAGAGCCAGCCAGCTGCTCTGAG 4164
DB 2 CCTACAGAGCCCTCGAGAGAGGTCCTTCCTGGAGAGCCAGCCAGCTGCTCTGAG 61

QY 4165 GAGGA--GAGCCAGAGGCGGTGAGCCCAACCCCTGCCAGCAGCAAGAGCCCTGCAATC 4221
DB 62 GAGGAAGAGCCGAGAGGAGGCGAGCCAGCTTCTCCAGCAGCAAGAGCCCTGCAATC 121

QY 4222 CAGACAGATCCAGAGGCGCGCTTCAGCTGCTGGGCAATGCTGGAGAGCCAGC 4281
DB 122 CAGATGAGATCCGAGAGGCGCGCTTCAGCTGCTGGGCAATGCTGGAGAGCCAGC 181

QY 4282 GGGCGGCGCTGCGCCAGAGATCATCCCTACCAACCCAGGAGCAAGAGAGCTGCTG 4341
DB 182 GGGCGGCGCTGCTGCTAGATGCTTCCCTACCAACCTGAGGAGCAAGAGAGCTGCT 241

QY 4342 CGGGAATAGAGGCGCTCAAGGCGCTGCGCCAGCCAGCCAGCTGCGCCAGCCAGC 4401
DB 242 AGAGAATAGAGGCGCTCAAGAGAGCTGAGCAACCCAGCAATCTGCGCCAGCCAGC 301

QY 4402 TACTCAGCCCGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4461
DB 302 TACTCAGCTCCCGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

QY 4462 CCTGCTGCGCGAGAGGCGCTTCTACTCAGATCTGAGGCTGAGAGGACTACTCTGCGAG 4521
DB 362 CCTCTTTGCGGAGAGGGAATCCTACTCAGAGCTGATGTGAAGGACTACTCTGCGAG 421

QY 4522 ATGTTGAGTGCCACCCAGTACCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 4581
DB 422 ATGCTGAGTGCCACCCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481

QY 4582 GAGAAATGATCATACCGAATACACCTGCTCAAGGCTCGTGGAGCTGCGGCAATGCAAG 4641
DB 482 GAGAAATGATGCTCACTGAGTACAACTGCTTAAGGTTATAGACCTGCGGAAATGCCCAG 541

QY 4642 AGCTCAGCAGAGAGAGGCTGCTGCTCAGACAGGTTCAAGGACTACCTAGAGACCATG 4701
DB 542 AGTCTGACCAAGAGAGGTCAGGCGCTGAGAACTTCAAGACTACTGAGAGACCATG 601

QY 4702 GCTCCAGAGCTCCTGAGAGGCGCAGGGGCTGTTCCACAGAGAGATCTGGGCAATCGGT 4761
DB 602 GCTCCAGAGACTCCTGGAAGGTCACCGGCTGTTCCACAGAGAGACA--TTGGGCTATGCT 659

QY 4762 GTGACAGCTTCATGCTGAGCGCGAGTACCGGCTGAGCAGAGGCTGACCGGAC 4821
DB 660 GTACAG-CTTCATTTATGCTGAGTGGGAGTA-CCAGAGAGAGAGGGGAGCTCTGTA- 716

QY 4822 CTGAGAGAGGAGCTGCGCAGG 4843
DB 717 CTGGAGAAAGGCTTGGCAGGG 738

RESULT 13

B1916956
LOCUS
DEFINITION
60317770F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242121 5',
mRNA sequence.
B1916956
EST.
B1916956.1 GI:16180910
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov/
Plate: LLNL1610 row: k column: 18
High quality sequence stop: 477.
Location/Qualifiers
1. 477
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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 8.7%; Score 453; DB 12; Length 477;
Best Local Similarity 99.6%; Pred. No. 1.2e-83;
Matches 475; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 3637 GTGACACTGGCTGCCAGGTGTGAGCCCA-GCCAGCTGCCAGCCACCTGGAGCAA-AG 3694
DB 1 GTGACACTGGCTGCCAGGTGTGAGCCCA-GCCAGCTGCCAGCCACCTGGAGCAAAG 60

QY 3695 ACCGAGCCCCCTGGAGAGCAGCCGCTGCTCATCTCTGCCACCTCAAGAACTTCC 3754
DB 61 ACCGAGCCCCCTGGAGAGCAGCCGCTGCTCATCTCTGCCACCTCAAGAACTTCC 120

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DB 121 AGCTTCTGACCATCTGCTGGTGTGCTGAGACCTGGGTGTGTACCTGCGAGGTGA 180

QY 3815 GCAATGCTCGGGACAGTGAACACACCGGCGCTCTCCGGAAGGAGGAGCGCCCTCAT 3874
DB 181 GCAATGCTCGGGACAGTGAACACACCGGCGCTCTCCGGAAGGAGGAGCGCCCTCAT 240

QY 3875 CTTGCCATGCCCGATATCGGGAGGTGTACCGGAGTGGGTGCTGCTGCTGGAAGC 3934
DB 241 CTTGCCATGCCCGATATCGGGAGGTGTACCGGAGTGGGTGCTGCTGCTGGAAGC 300

QY 3935 CCGTGAATCTACGGCCCTGTGTACCTTGTGAGTGTGACGCTAGAGGCGGAGCT 3994

Db	301	CCGTGGAATCCTACGGCCCTGTGAACCTACATGTGTCAGTGCAGCTAGAAGCGGCAGCT	360
QY	3995	GGACACACACTGGGCTCCGACATCTTTGACTGTGTCTACTCTGACAGCAAGCTCTCCCGG	4054
Db	351	GGAGCACACTGGGCTCCGACATCTTTGACTGTGTCTGCTCTGACAGCAAGCTCTCCCGG	420
QY	4055	GTGSCACCTACACCTTCCGACCGCATGTGTGAGCAAGGACAGGAATGGTGCCCTACA	4111
Db	421	GTGSCACCTACACCTTCCGACCGCATGTGTGAGCAAGGACAGGAATGGTGCCCTACA	477

[illegible]

BOOKS RECEIVED

ORGANISM Homo sapiens (human)

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 517)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsuksuna, A., Baia, G.S., Simpson, D.H., Brunschein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

JOURNAL
MEDLINE
PUBMED
COMMENT

Lucwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimposon@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml.pl?l1=MR2&t3=MR2-H1160-190101-013-e11&t3=2001-01-19&t4=1>
Seq primer: puc 18 forward
High quality sequence stop: 355.

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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1160"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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Query Match 8.3%; Score 434; DB 12; Length 517;
Best Local Similarity 94.5%; Pred. No. 5.3e-51;

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508 AAGCCTCTTACCATCTCTGATGGT-CATCCTTCCCCGGGACACATTAAATCTGGCGACTTT 450

QY 361 GTGACCTGGTACAAAGGACAGCGTCCAGCTGGTGGAGACACCCGCTTAGCCAGCAAA 420
Db 361 GTGACCTGGTACAAAGGACAGCGTCCAGCTGGTGGAGACACCCGCTTAGCCAGCAAA 420
QY 421 GAAGGACCAACATATCTCCCTGGTGTGAGGCATGTGGCTCCAAAGGATGCGGGGTTTAC 480
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QY 481 ACCTGCTGGCCCAAAACACTGGTGGCCAGAGTGTCTGCAAGGACAGAGCTGCTGGTCTT 540
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Db 601 TATGAGGTCAAGGAGAGAGATTGGAAGGGGCGTGTGGCTTCGTAAGAAAGTGCACAC 660
QY 661 AAAGGAAACAAGATCTTGTGCGCTGCGCAAGTTCATCCCGCTACGGAGAGAACTCGGGCC 720
Db 661 AAAGGAAACAAGATCTTGTGCGCTGCGCAAGTTCATCCCGCTACGGAGAGAACTCGGGCC 720
QY 721 CAGGCATACAGGAGAGCGAGACATCTGCGCGCGCTGAGCCACCGCGCTGGTCAACGGGCGTG 780
Db 721 CAGGCATACAGGAGAGCGAGACATCTGCGCGCGCTGAGCCACCGCGCTGGTCAACGGGCGTG 780
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QY 841 GAGCTGCTGGACCGCGCTGTACAGGAAGGGCGTGTGAGCGAGGCGGAGGTCAAGAGTCTAC 900
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QY 961 ATAAAGCCCTCTAAACATCTGATGCTGATCTCTGCGGGGAAGACATTAATAATCTGGAC 1020
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Db 1141 GCCATGGGTGTCATCTCTCATCTGAGCTGACCTGCTCATCCCATTTGCGGGAGAGT 1200
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QY 1261 GCCACCTCAGGAGAGCGCAAGACTTCATCAGGCTAGCTGAGAGAGCCCTCAG 1320
Db 1261 GCCACCTCAGGAGAGCGCAAGACTTCATCAGGCTAGCTGAGAGAGCCCTCAG 1320
QY 1321 GCCCGGCTAGTGGGGCCAGTGCCTCTCCACCCCGTGGTTCTGAAATCCATGCTGG 1380
Db 1321 GCCCGGCTAGTGGGGCCAGTGCCTCTCCACCCCGTGGTTCTGAAATCCATGCTGG 1380
QY 1381 GAGGAGGCCCTTCATCAACACAGCAGCTCAAGTTCTCTCTGGGCCGAAAGTCCGCTGG 1440
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RESULT 2
 US-10-274-978-1
 ; Sequence 1, Application US/10274978
 ; Patent No. 6670164
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui, et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO00927-CIP-DIV
 ; CURRENT APPLICATION NUMBER: US/10/274,978
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: 09/858,664
 ; PRIOR FILING DATE: 2001-05-17
 ; PRIOR APPLICATION NUMBER: 09/711,134
 ; PRIOR FILING DATE: 2000-11-14
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 5207
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-274-978-1

Query Match 100.0%; Score 5207; DB 4; Length 5207;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2461	Db	GCCAAAGCAAGCCCCCATTTGGACTCTAAGATGGGCTTGAGACATCTCTCTCTGG	2520
2521	QY	AGGCCAAACCCGGCCCTTGCACTTCCCAAGGTACGCTCCAGGGAGCTCTTCCAA	2580
2521	Db	AGGCCAAACCCGGCCCTTGCACTTCCCAAGGTACGCTCCAGGGAGCTCTTCCAA	2580
2581	QY	GTGAGCTCCCTCAGGTGGGCTCTCCAGGTGGGCAAGAGCTTGGCCCTCCTTGAT	2640
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2641	Db	GGGAGGCTGGACCCAGAGGCTGAGGATCTGTCGACTCCACACCACTTGCAGCG	2700
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3061	Db	GATCGGAGGGGGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGCTACCTC	3120
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3301	Db	ACAGAGGAGTCAGAGGATGTGACGCGCTGTGTGCAGAGGTGCGTGGGCAGGAAGCGC	3360
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Qy	61	GTTCATTGAAGAGTACTCTCTAACTGTCAAGAACTGGGCGGTCAAGATGGGTCGT	120
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Qy	901	ATCCAGACAGCTGGTGGAGGGGCTGCATACCTGACACAGCCATGGCTTCTCCACTGGAC	960
Db	901	ATCCAGACAGCTGGTGGAGGGGCTGCATACCTGACACAGCCATGGCTTCTCCACTGGAC	960
Qy	961	ATAAAGCCCTCTAAACATCTGATGGTGCATCTCTGCCCGGGAAGACATTAATAATCTGCAC	1020
Db	961	ATAAAGCCCTCTAAACATCTGATGGTGCATCTCTGCCCGGGAAGACATTAATAATCTGCAC	1020
Qy	1021	TTTGGCTTGGCCAGAAACATACCCCAAGCAGCTGAGTTCAGCCAGTACGGCTCCCTC	1080
Db	1021	TTTGGCTTGGCCAGAAACATACCCCAAGCAGCTGAGTTCAGCCAGTACGGCTCCCTC	1080
Qy	1081	GAGTTCGTCTCCCGCCAGATCATCCAGCAGAAACCTCTGTGAGGGAAGCCTTCGACATTGG	1140

1081	DB		GAGTTCGTCTCCCCGAGATCATCCAGCAAGACCCCTGTGACGAAGCCTCCGACATTGG	1140
1141	QY		GCCATGGGTGCATCTCTTAACCTCAGCGCTGACCTGTCTCATCCCAATTGCGCGAGAGT	1200
1141	DB		GCCATGGGTGCATCTCTTAACCTCAGCGCTGACCTGTCTCATCCCAATTGCGCGAGAGT	1200
1201	QY		GACCGTGCACCCCTCTGAAGTCTCTGGAGGGCGGTGTCTATGGAGCAGCCCATGGCT	1260
1201	DB		GACCGTGCACCCCTCTGAAGTCTCTGGAGGGCGGTGTCTATGGAGCAGCCCATGGCT	1260
1261	QY		GCCCACTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAG	1320
1261	DB		GCCCACTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAG	1320
1321	QY		GCCCGGCTAGTGGGCCCAAGTGCCTCTCCACGCCCTGTCTCTGAAATCCATGCTCGG	1380
1321	DB		GCCCGGCTAGTGGGCCCAAGTGCCTCTCCACGCCCTGTCTCTGAAATCCATGCTCGG	1380
1381	QY		GAGGAGCCCACTTCATCAACACCAAGCAGCTCAAGTTCCTCTGCGCCGGAAGTGCCTGG	1440
1381	DB		GAGGAGCCCACTTCATCAACACCAAGCAGCTCAAGTTCCTCTGCGCCGGAAGTGCCTGG	1440
1441	QY		CAGCGTTCCTGTATGAGCTACAAAGTCCATCTCGTGTATGGCTCCATCCCTGAGCTGCTG	1500
1441	DB		CAGCGTTCCTGTATGAGCTACAAAGTCCATCTCGTGTATGGCTCCATCCCTGAGCTGCTG	1500
1501	QY		CGGGGCCACCCGACAGCCCTCCCTGGCGGTAGCCCGGCACTCTGCAGGGACATCTGGT	1560
1501	DB		CGGGGCCACCCGACAGCCCTCCCTGGCGGTAGCCCGGCACTCTGCAGGGACATCTGGT	1560
1561	QY		GGCTCTCCAGTTCTCTCTCTCTGTGACAAAGAGCTGCGCCCATTTGGCCGGGCTAAG	1620
1561	DB		GGCTCTCCAGTTCTCTCTCTCTGTGACAAAGAGCTGCGCCCATTTGGCCGGGCTAAG	1620
1621	QY		TCACTGCGACCCCTCCCGGTGACACTACCACTGCTGCAACCCCGGGGCTTCCTGGCGG	1680
1621	DB		TCACTGCGACCCCTCCCGGTGACACTACCACTGCTGCAACCCCGGGGCTTCCTGGCGG	1680
1681	QY		CCCTCGGCAGCTGCTGTGAGGAAGCGAGGCGCAGTGAGCGCTCCACCGAGGGCCCCAGCT	1740
1681	DB		CCCTCGGCAGCTGCTGTGAGGAAGCGAGGCGCAGTGAGCGCTCCACCGAGGGCCCCAGCT	1740
1741	QY		CCGCTGCATCTCCGAGAGTGCAGGGCACCGCGCGCCAGGGCTCGGTGCCCCGGGCAC	1800
1741	DB		CCGCTGCATCTCCGAGAGTGCAGGGCACCGCGCGCCAGGGCTCGGTGCCCCGGGCAC	1800
1801	QY		AGCGTCATCCGACGCTGTTCTACCAACAGCGCGGTGAGAGCCCTGAGCAGCGGGGCCCTG	1860
1801	DB		AGCGTCATCCGACGCTGTTCTACCAACAGCGCGGTGAGAGCCCTGAGCAGCGGGGCCCTG	1860
1861	QY		GCCCCGGGAGCAGCGGCGACCCGGCCCGCGCGGGCACTGTCTGAAGGCGGCTACATT	1920
1861	DB		GCCCCGGGAGCAGCGGCGACCCGGCCCGCGCGGGCACTGTCTGAAGGCGGCTACATT	1920
1921	QY		GCGGGGCGTGTGCAGGCTGTGCGGAGGCACTGATGGAGCACCGCGCTGTCTGGAGGAGGAG	1980
1921	DB		GCGGGGCGTGTGCAGGCTGTGCGGAGGCACTGATGGAGCACCGCGCTGTCTGGAGGAGGAG	1980
1981	QY		GCGCGCAGGGAGGAGCAGGCGCACCTCTCTGGCCAAAGCCCCCTCATTCGAGACTGCCCTTC	2040
1981	DB		GCGCGCAGGGAGGAGCAGGCGCACCTCTCTGGCCAAAGCCCCCTCATTCGAGACTGCCCTTC	2040
2041	QY		CGGCTGCTGCCTCTGCGACCCCACTTGGCCCCCTGGCCACAGCCACTCTCTGGAAATGAC	2100
2041	DB		CGGCTGCTGCCTCTGCGACCCCACTTGGCCCCCTGGCCACAGCCACTCTCTGGAAATGAC	2100
2101	QY		TCTCCGAGCACCCCGCCCTCTCTCGGAGGCTGCGGTGAGGCA CAGGACTGCTTCA	2160
2101	DB		TCTCCGAGCACCCCGCCCTCTCTCGGAGGCTGCGGTGAGGCA CAGGACTGCTTCA	2160
2161	QY		GCCCCCTCCGGGGGGCCCCCTATAGGGACAATGGGGCACCCCTCAGGGCTCCAAAGCAGCTT	2220

2161	Db	GCCCCCTCCGGGGGGGCCCTTATCAGGACATGAGGGCACTTCAGGGTCCAAAGACGCTT	2222
2221	Qy	CCATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCCGACAGCCCT	2280
2221	Db	CCATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCCGACAGCCCT	2280
2281	Qy	TGGGGGACGACGACCCCTTTCTGCGACCCCAAGCAGGGTCTTCCGCCACGAGGGGTGC	2340
2281	Db	TGGGGGACGACGACCCCTTTCTGCGACCCCAAGCAGGGTCTTCCGCCACGAGGGGTGC	2340
2341	Qy	AGCCCCACCCAGCAGTTGCCCATGCCCCCTCTCGGCTCCCTTCCCTCCAGGATCTTGCAAA	2400
2341	Db	AGCCCCACCCAGCAGTTGCCCATGCCCCCTCTCGGCTCCCTTCCCTCCAGGATCTTGCAAA	2400
2401	Qy	GAGGCCCTTAGTACCTCBAAGCCCTCTCTGGGACAGCCCGACGACCCCTCGCCCT	2460
2401	Db	GAGGCCCTTAGTACCTCBAAGCCCTCTCTGGGACAGCCCGACGACCCCTCGCCCT	2460
2461	Qy	GCCAAAGCAAGCCCCCATTTGACATCTAAGATGGGCCCTTGGAGACATCTCTCTTCTGGG	2520
2461	Db	GCCAAAGCAAGCCCCCATTTGACATCTAAGATGGGCCCTTGGAGACATCTCTCTTCTGGG	2520
2521	Qy	AGGCCAAAGCCGGCCCTGCAGTTCGCCAGGGTCAGCCTCCACAGCGAGCTCTTCCCAA	2580
2521	Db	AGGCCAAAGCCGGCCCTGCAGTTCGCCAGGGTCAGCCTCCACAGCGAGCTCTTCCCAA	2580
2581	Qy	GTGAGTCCCTCAGGGTGGCTCCTCCAGGTGGGCACAGAGCCTGGGCCCTCCCTCGAT	2640
2581	Db	GTGAGTCCCTCAGGGTGGCTCCTCCAGGTGGGCACAGAGCCTGGGCCCTCCCTCGAT	2640
2641	Qy	GCGGAGGGCTGACCCACAGAGGCTGAGGATCTGCTCGACTCCACACCCACCTTCACAGCG	2700
2641	Db	GCGGAGGGCTGACCCACAGAGGCTGAGGATCTGCTCGACTCCACACCCACCTTCACAGCG	2700
2701	Qy	CTCAGGAAACAGGTGACCATGCGCAAGTTCTCCTGGGTGGTGGGGGTACGACAGGC	2760
2701	Db	CTCAGGAAACAGGTGACCATGCGCAAGTTCTCCTGGGTGGTGGGGGTACGACAGGC	2760
2761	Qy	GTGGCTGGCTATGGCACCTTTGCCCTTGGTGGAGATGACAGGGGGCATGCTGGGGCAGGGG	2820
2761	Db	GTGGCTGGCTATGGCACCTTTGCCCTTGGTGGAGATGACAGGGGGCATGCTGGGGCAGGGG	2820
2821	Qy	CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGCAGGAGGAG	2880
2821	Db	CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGCAGGAGGAG	2880
2881	Qy	GCCAGGGCTGAGTCCCAGTCGGAGGACACAGAGGGCCAGGGCTGAGAGGCCACTGCCCC	2940
2881	Db	GCCAGGGCTGAGTCCCAGTCGGAGGACACAGAGGGCCAGGGCTGAGAGGCCACTGCCCC	2940
2941	Qy	CAGGTCAGTCAAGGCCCTGTGCCTGAGGTGCGAGGGCTCCACACAGGAGCTTCAGAG	3000
2941	Db	CAGGTCAGTCAAGGCCCTGTGCCTGAGGTGCGAGGGCTCCACACAGGAGCTTCAGAG	3000
3001	Qy	CCACCCCATGGGAGGACATCGGGCAGGCTCCCTGGTGCAGATCCGGGACCTGTGAGGT	3060
3001	Db	CCACCCCATGGGAGGACATCGGGCAGGCTCCCTGGTGCAGATCCGGGACCTGTGAGGT	3060
3061	Qy	GATCGGAGGGGCGGACAAATATCCCTGGACATTCGAGGTGGACCCCGGCTACCTC	3120
3061	Db	GATCGGAGGGGCGGACAAATATCCCTGGACATTCGAGGTGGACCCCGGCTACCTC	3120
3121	Qy	AACTCTCTCAGACCTGTACGATATCAAGTACCTCCCATCGAGTTTATGATCTTCAGAAA	3180
3121	Db	AACTCTCTCAGACCTGTACGATATCAAGTACCTCCCATCGAGTTTATGATCTTCAGAAA	3180
3181	Qy	GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCCCTGGCTGAGGAGGAGCTGGCCGAG	3240
3181	Db	GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCCCTGGCTGAGGAGGAGCTGGCCGAG	3240
3241	Qy	TTCCCGAGGCCACGCTGGCCCTGGCCAGGTTAACTGGGCCCCCGACGAGGCTGGAGATC	3300
3241	Db	TTCCCGAGGCCACGCTGGCCCTGGCCAGGTTAACTGGGCCCCCGACGAGGCTGGAGATC	3300

QY	3301	ACAGAGGATCAGAGGATGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCGC	3360
DB	3301	ACAGAGGATCAGAGGATGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCGC	3360
QY	3361	AAATGGTCCCTCGCCGTCACGCAAGCCTCTTCCACTTCCCTGGGAGGCACTGCGCGTGGAT	3420
DB	3361	AAATGGTCCCTCGCCGTCACGCAAGCCTCTTCCACTTCCCTGGGAGGCACTGCGCGTGGAT	3420
QY	3421	GAGCCTGCAGAGCTGGGGCTGGGTGAGAGAGTGAAAGGCTCCGTGGAGGACATCTCCCGG	3480
DB	3421	GAGCCTGCAGAGCTGGGGCTGGGTGAGAGAGTGAAAGGCTCCGTGGAGGACATCTCCCGG	3480
QY	3481	ATCCTGAAGGCGAGGCCGGAAGGTCTGGGAAGAAGAGGGGCCCCCCAGGAAGAAGCAGGC	3540
DB	3481	ATCCTGAAGGCGAGGCCGGAAGGTCTGGGAAGAAGAGGGGCCCCCCAGGAAGAAGCAGGC	3540
QY	3541	CTTGTCTTCTTCGGGCTCTCAGGTCTGAAGAGCTGGGACCGGACGCGGACATCTCTAAGG	3600
DB	3541	CTTGTCTTCTTCGGGCTCTCAGGTCTGAAGAGCTGGGACCGGACGCGGACATCTCTAAGG	3600
QY	3601	GAGCTCTCAGATGAGACTGTGTCTTGGGCCAGTCAGTGACACTGGCCCTGCCAGGTGTCA	3660
DB	3601	GAGCTCTCAGATGAGACTGTGTCTTGGGCCAGTCAGTGACACTGGCCCTGCCAGGTGTCA	3660
QY	3661	GCCAGGCACTGCCCAGGCCACTTGGAGCAAAAGACGAGGCCCTCTGGAGAGCAGCAGC	3720
DB	3661	GCCAGGCACTGCCCAGGCCACTTGGAGCAAAAGACGAGGCCCTCTGGAGAGCAGCAGC	3720
QY	3721	CGTGTCTCATCTCTGCCACCTCAAGAACTTCCAGCTTTCGACCATCTCGTGTGTGTG	3780
DB	3721	CGTGTCTCATCTCTGCCACCTCAAGAACTTCCAGCTTTCGACCATCTCGTGTGTGTG	3780
QY	3781	GCTGAGGACCTGGGTGTGTACACCTGACGCTGAGCAATGGCTGGGACAGTGACCAC	3840
DB	3781	GCTGAGGACCTGGGTGTGTACACCTGACGCTGAGCAATGGCTGGGACAGTGACCAC	3840
QY	3841	ACGGGGCTCTCCGGAAGGACAGAGCGCCCTCATCTTCGCCATGCCCGATATCGGGAG	3900
DB	3841	ACGGGGCTCTCCGGAAGGACAGAGCGCCCTCATCTTCGCCATGCCCGATATCGGGAG	3900
QY	3901	GTGTACGGGATGGGGTGTCTGTCTTGGAAAGCCGTGGAACTCTACGGCCCTGTGACC	3960
DB	3901	GTGTACGGGATGGGGTGTCTGTCTTGGAAAGCCGTGGAACTCTACGGCCCTGTGACC	3960
QY	3961	TACATTGTGTCAGTGCAGCCTAGAAGCGGCACTGGACCACTGGCTCCGACATCTTT	4020
DB	3961	TACATTGTGTCAGTGCAGCCTAGAAGCGGCACTGGACCACTGGCTCCGACATCTTT	4020
QY	4021	GACTGTGTACTCTACACGACAGCTCTCCGGGGTGCACCTACACCTTCGGACAGCA	4080
DB	4021	GACTGTGTACTCTACACGACAGCTCTCCGGGGTGCACCTACACCTTCGGACAGCA	4080
QY	4081	TGTGTGACAAGGCAAGGAATGGTCCCTACAGACAGCCCTCGGACAAAGTCTCTCTGGGA	4140
DB	4081	TGTGTGACAAGGCAAGGAATGGTCCCTACAGACAGCCCTCGGACAAAGTCTCTCTGGGA	4140
QY	4141	GGGCCACAGCACTGGCTCTTCAGAGAGAGAGCCAGGGGCGGTACGCCAACCCCTGCC	4200
DB	4141	GGGCCACAGCACTGGCTCTTCAGAGAGAGAGCCAGGGGCGGTACGCCAACCCCTGCC	4200
QY	4201	AGCACAAAGACCTTCGCATTCACAGACAGATCCAGAGGGGCCGCTTTCAGCGTGGTGGG	4260
DB	4201	AGCACAAAGACCTTCGCATTCACAGACAGATCCAGAGGGGCCGCTTTCAGCGTGGTGGG	4260
QY	4261	CAATGCTGGAGCAAGGCCAGCGGGCGGCGCTGGCGCCAGATCATCTCCCTACACCCC	4320
DB	4261	CAATGCTGGAGCAAGGCCAGCGGGCGGCGCTGGCGCCAGATCATCTCCCTACACCCC	4320
QY	4321	AAGGACAAGACAGCAGTGTGCGGAATACAGAGGCCCTTCAAGGGGCTTCGCGCAACCCGAC	4380
DB	4321	AAGGACAAGACAGCAGTGTGCGGAATACAGAGGCCCTTCAAGGGGCTTCGCGCAACCCGAC	4380

QY 4381 CTGCCCCAGTGCACGAGCCTACCTCAGCCCCCGCCACCTGGTCTCATCTTGGAGCTG 4440
DB 4381 CTGCCCCAGTGCACGAGCCTACCTCAGCCCCCGCCACCTGGTCTCATCTTGGAGCTG 4440
QY 4441 TGTCTTGGCCCCGAGTGTCTCCCTGCTTGGCGGAGAGGCGCTCTCTCTCAAGATCTGAG 4500
DB 4441 TGTCTTGGCCCCGAGTGTCTCCCTGCTTGGCGGAGAGGCGCTCTCTCTCAAGATCTGAG 4500
QY 4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCACCCAGTACCTGTCACAAACCCAGCAGATC 4560
DB 4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCACCCAGTACCTGTCACAAACCCAGCAGATC 4560
QY 4561 CTGCACCTGAGCTGAGTGTCCGAGACATGATCATCCGATATCATCCGATCTCTCAAGTTC 4620
DB 4561 CTGCACCTGAGCTGAGTGTCCGAGACATGATCATCCGATATCATCCGATCTCTCAAGTTC 4620
QY 4621 GTGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAGTGTCTGCTCCCTCAGACAGTTC 4680
DB 4621 GTGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAGTGTCTGCTCCCTCAGACAGTTC 4680
QY 4681 AAGGACTACTAGAGACATGCTCCAGAGCTCTCCGAGGCTCTCCGAGGCTGTTCACAG 4740
DB 4681 AAGGACTACTAGAGACATGCTCCAGAGCTCTCCGAGGCTCTCCGAGGCTGTTCACAG 4740
QY 4741 ACAGACATCTGGGCCATCGGTGTGACAGCTTTCATCATCTGAGCGCGAGTACCCGGTG 4800
DB 4741 ACAGACATCTGGGCCATCGGTGTGACAGCTTTCATCATCTGAGCGCGAGTACCCGGTG 4800
QY 4801 AGCAGCGAGGTGCACGCGACCTGCAGAGAGTCTCCGAGGCTGTTCACAG 4860
DB 4801 AGCAGCGAGGTGCACGCGACCTGCAGAGAGTCTCCGAGGCTGTTCACAG 4860
QY 4861 CGTGTACGCGGGGTGTCTCCGCGGCGCGCGTGTCTTCTGCGCAGCACTCTGTGCGCC 4920
DB 4861 CGTGTACGCGGGGTGTCTCCGCGGCGCGCGTGTCTTCTGCGCAGCACTCTGTGCGCC 4920
QY 4921 CAGCCCTGGGCGCGCTCTCCGCGGCTGCTGAGTCTGCTGAGTCTGCTGAGTCTGCTGAG 4980
DB 4921 CAGCCCTGGGCGCGCTCTCCGCGGCTGCTGAGTCTGCTGAGTCTGCTGAGTCTGCTGAG 4980
QY 4981 GSCCGGCTGTGTGGCGGCGCGCTGAGCTTCTTCTGCGCGGCTGCTGAGTCTGCTGAG 5040
DB 4981 GSCCGGCTGTGTGGCGGCGCGCTGAGCTTCTTCTGCGCGGCTGCTGAGTCTGCTGAG 5040
QY 5041 GTGCGCAATCGGAGAGAGCGCGCTGCTGAGTCTGCTGAGTCTGCTGAGTCTGCTGAG 5100
DB 5041 GTGCGCAATCGGAGAGAGCGCGCTGCTGAGTCTGCTGAGTCTGCTGAGTCTGCTGAG 5100
QY 5101 CGTGTAGGCTGCGCGGCGCACACCTTGTCTCCCGCTGGGGTGTGCTGAGTCTGCTGAG 5160
DB 5101 CGTGTAGGCTGCGCGGCGCACACCTTGTCTCCCGCTGGGGTGTGCTGAGTCTGCTGAG 5160
QY 5161 CAATTAACCGCAGCGCGGAG 5207
DB 5161 CAATTAACCGCAGCGCGGAG 5207

RESULT 4
US-09-159-385-4
; Sequence 4, Application US/09159385
; Patent No. 5958748
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: PH-569
; CURRENT APPLICATION NUMBER: US/09159385
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) .. (1353)
US-09-159-385-4

Query Match 3.4%; Score 178.2; DB 2; Length 1429;
Best Local Similarity 53.5%; Pred. No. 7.9e-27;
Matches 437; Conservative 0; Mismatches 353; Indels 27; Gaps 2;

QY 601 TATGAGTCAAGGAGGAGATTTGGAAGGGCGTGTGGCTTCGTAAAAAGAGTGCAGCAC 660
DB 46 TATGAGTGGGAGGAGAGCTTTGGCAGTGGCCAAATTTGCCATCGTGCACAGTGCAGCAG 105
QY 661 AAAGGAAACAAGATCTTGTGGCGTCCCAAGTTCATCCCTTACGAGAGCAGAACT- 714
DB 106 AAGGCAACGGGATGAGTATGACGCAAGTTCATCAAGAGCGCGCTGCCATCCAGC 165
QY 715 -----CGGCGCCAGGCATACAGGAGCGAGACATCTTGGCGCGCTGAGC 759
DB 166 CGGCGCGTGTGAGCGGAGGAGATCGAACGCGAGTGCATCTTCCGCGAGATCCGC 225
QY 760 CACCCCGCTGTGTCAGGGGCTGCTGAGCCAGTTCGAGACCCGCGAAGACCTCATCTCATC 819
DB 226 CACCCCAACATCAATAACACTGCATGACGTGTTTCAGAACAAAGACAGATGTGGTCTGATC 285
QY 820 CTGAGAGCTGTCTCATCCGAGAGCTGCTGACCGCTGTACAGGAAGGCGGTGGTGAAG 879
DB 286 CTGAGAGCTGTGTCGCGTGGCGAGCTTTTCGACTTCTTGGCGGAGAGAGTCAATTGACG 345
QY 880 GAGGCGGAGGTCAAGGTCTACATCCAGCAGCTGTGTGAGGGGCTGCACATCTGTCAGCAGC 939
DB 346 GAGGATGAGGCGACGCGAGTTCCTCAAACTAATCTAGACGTGTCCACTACCTGCACTCC 405
QY 940 CATGCGGTTCCTCCACTGGAGTAAAGCCCTCTAAACATCTGATGGT- 993
DB 406 AAGCCATCGCACACTTTGAGCTGAAGCGCGAGAACATCATGTTGCTGGACACAGCA 455
QY 994 GCGCGGGAAGACATTAATAATCTGCGACTTTGGCTTTTCCCGAGAACATCACCCAGCAGAG 1053
DB 466 GCGAGCGCGCGCTTAAGCTCATGACTTTGGCATTCGCGACAGGATCGAGGCTGGCAGC 525
QY 1054 CTGCGAGTTCAGCAGTACGCTCCCTGAGTGTGGTCTCCCGCGAGATCATCCAGCAGAAC 1113
DB 526 GAGTTCAAGAAACATCTTTGGCAGACCCGAGTGTTCGCCCCCGAGATCTGTAACATGAG 585
QY 1114 COTGTGAGCGAAGCTCCGACATTTGGGCCCATGGGTGTCTATCTCTACCTCAGCCTGAC 1173
DB 586 CCACCTTGGCTTGGAGGCTGACATGCGAGCATTTGGCGTCACTACCTACATCTCTGAGC 645
QY 1174 TGCTCATCCCATTTGCGGCGAGTGCAGCGTGCACCCCTCTGAGCCTCTGGAGGGG 1233
DB 646 GAGGCTTCCCATTTCTGGGCGAGACCAAGAGAGAGCTGACAGACATCTCAGCAGTG 705
QY 1234 CGCTGTGTCAGGAGCGCCCATGGCTGCCCATCTCAGCGAAGACGCGCAAGACTTTCATC 1293
DB 706 AACTATGACTTTGATGAGGAATATCTCAGCAGCAGCAGCAGGCTGGCCAGGACTTTCATC 765
QY 1294 AAGGCTAGCTGCAGAGAGCGCCCTCAGCGCGCGCTAGTGGCGCCAGTGCCTCTCCAC 1353
DB 766 CGCAGGCTGTGGTCAAGACCCCAAGAGAGAGATGACCATCCACAGAGCCTGGAGCAT 825
QY 1354 CCCTGGTTCTTGAATTCATGCTCTGCGAGAGAGGCC 1390
DB 826 TCCTGGATCAAGGTGCGCAGGCGGAGGAGCGGCGCC 862

RESULT 5
US-09-186-277-4
; Sequence 4, Application US/09186277
; Patent No. 6171841

DB	766	CGCAGGCTGTGTCAAAGACCCCAAGAGGAGATGCCATCGCACAGAGCTGGAGCAT	825
QY	1354	CCCTGGTTCTTGAATTCATGCTCGGAGGAGGCC	1390
DB	826	TCCTGGATCAAGTGCGCAGCGCGAGGACGGCGCC	862
 RESULT 6 US-09-159-385-3			
; Sequence 3, Application US/09159385			
; Patent No. 5958748			
; GENERAL INFORMATION:			
; APPLICANT: AKIRA, SHIZUO			
; APPLICANT: KAWAI, TARO			
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE			
; FILE REFERENCE: PH-569			
; CURRENT APPLICATION NUMBER: US/09/159,385			
; CURRENT FILING DATE: 1998-09-23			
; EARLIER APPLICATION NUMBER: JF97/261589			
; EARLIER FILING DATE: 1997-09-26			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 2132			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (94)..(1455)			
US-09-159-385-3			
 Query Match 3.3%; Score 173.4; DB 2; Length 2132; Best Local Similarity 53.3%; Pred. No. 8.le-26;			
Matches 431; Conservative 0; Mismatches 351; Indels 27; Gaps 2;			
QY	580	CGGAGGAGCTGCACCTCTTATGAGGTCAAGGAGGAGATTGGAAAGGGCGTGTTCG	639
DB	109	CAGGAGACGCTGGAGGACCATTATGATGGGGGAGGAGCTGGCAGCGCCAGTTGCG	168
QY	640	TTCGTAAGAAGATGCGAGCACAAAGAAACAAGATCTTGTGCGCTGCCAACGTTTCATCCC-	698
DB	169	ATCTGCGGAAGTCCCGCAGAGGSCACGGCAGGAGTAGCAGCACCAGTTTCATCAAG	228
QY	699	-----CCTACGGACGAACTCGGCCCAGGCATACAGGAGCGA	738
DB	229	AAGCGCGCTGTTCATCCAGCGCGCTGGGTGAGCGCGGAGGAGATCGACGGGAGTG	288
QY	739	GACATCTGCGCGGTGAGCACACCGCTGTCACGGGGCTGCTGGACAGCTTTGAGACC	798
DB	289	AACATCTGCGGAGATCCGGCACCCCAACATCATCCCTGCACGACATCTTCGAGAAC	348
QY	799	CGAAGACCTCATCTCATCTCTGGAGCTGTCTCATCCGAGGAGCTCTCGACCGCTG	858
DB	349	AAGACGAGACTGTGTCTCATCTCTGAGCTGTGCTCTGCGGGAGCTCTTTGACTTCTG	408
QY	859	TACAGGAAGCGCGTGTGTCAGGAGGCGGAGGTCAAGGCTTACATCCAGCAGCTGGTGAG	918
DB	409	CGCGAGAAAGACTCGTGCAGCGGAGGACGAGGCCACCCAGTTCTCTCAAGCAGATCCTGAC	468
QY	919	GGGTGCACTTAACCTGCACAGCCATGGCGTTCTCCACTTGGACATAAGCCCTCTAAACATC	978
DB	469	GGCGTTCACTACCTGCACCTTAAGCGCATCGCACACTTTGACCTGAAGCGCGGAACATC	528
QY	979	CTGATGTGTGATCTCGTCCCGGGAAGAC-----ATTAAATCTGCACTTTGGCTTTGCC	1032
DB	529	ATGCTGTGACAAGAAGCTGCCAACCCACGAATCAAGCTCATGACTTCGGCATCGCG	588
QY	1033	CAGAACATACCCAGCAGAGCTGCAGTTTCACGTCAGTAGGCTCCCTCGAGTTGCTGCTCC	1092
DB	599	CACAAGATCAGGCGCGGGAACGAGTTTCAAGAACATCTTCGGCACCCCGAGTTTGTGCC	648
QY	1093	CCCAGATCATCCAGCAGAAACCCCTGTGAGCGAAGCCTCCGACATTTGGGCGATGGGTC	1152

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; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: 081356/0128
; CURRENT APPLICATION NUMBER: US/09/186,277
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(1353)
;
US-09-186-277-4

Query Match      3.4%; Score 178.2; DB 3; Length 1429;
Best Local Similarity 53.5%; Pred. No. 7.9e-27;
Matches 437; Conservative 0; Mismatches 353; Indels 27; Gaps 2;

QY      601  TATGAGTCAAGGAGGAGATTGAAGGGCGGTGTTGGCTTCGTAATAAAGATGCACGAC 660
DB      46   TATGAGATGGAGAGGAGCTTGGCATGTGCCAATTGCCATCGTGGCAAGTGCACGAG 105

QY      661  AAAGGAACAAAGATCTTGTGCGCTGCCAAAGTTTCATCCCCCTACGGAGCAGAACT----- 714
DB      106  AAGGGCAGCGGCATGGAGTATGCAGCAAGTTTCATCAAGAAGCGCGCCTGCCATCCAGC 165

QY      715  -----CGGGCCCGGCGATACAGGAGCGAGATCGAACCGAGGTGAGCATCTCGCGGAGATCCG 225
DB      166  CGGCGCGGTGTGACCGCGGAGAGATCGAACCGAGGTGAGCATCTCGCGGAGATCCG 225

QY      760  CACCCGTGTGTACCGGGCTGTGTGACCAAGTTTGAGACCCGCAAGACCTCATCTCATC 819
DB      226  CACCCCAACATCATAACTGTCATGACGTGTTCGAGAAACAAGACAGATGTGTTGCTGATC 285

QY      820  CTGAGAGCTGTGCTCATCCGAGGAGCTGTGGACCGCTGTACAGGAAGGGCGTGTGACG 879
DB      286  CTGAGAGCTGTGTCGGGTGCGAGCTTTCGACTTCTCGCGGAGAGGAGTCAATTGACG 345

QY      880  GAGCCGAGGTCAAGGTCTATATCCAGCAGCTGTGTGGAGGGCTGCACTACTGTCAACG 939
DB      346  GAGGATGAGGCCACCGAGTTCCTCAACAAATCTCTAGACGGTGTCCACTACTGTCACTCC 405

QY      940  CATGCGCTTCTCCACCTGGACATAAAGCCCTCTAACTCATCTCTGATGGT-----GCATCCT 993
DB      406  AAGCGCATCGCACTATTGACTGTAAGCCCGAGAACATCATATGTTGTGGACAGCAGCA 465

QY      994  GCCCGGGAAGACATTAATATCTCGCATTTGGCTTTGCCAGAACATCAACCCAGCAGAG 1053
DB      466  GCCAGCCCCGCATTAAGCTCATCGACTTTGGCATCGCGCAAGGATCGAGGCTGGCAGC 525

QY      1054  CTGCGAGTTCAGCCAGTACGGCTCCCTCGTAGTTTCGTCTCCCGCGAGATCATCCAGCAGA 1113
DB      526  GAGTTCAGAACATCTTTGGCACACCGAGTTTGTGCCCCCGAGATCGTGAATATGAG 585

QY      1114  CCTGTGAGCGAAGCCTCCGACATTTGGGCCATTTGGGTGTATCTCTTACTCAGCTTGACC 1173
DB      586  CCACTTGGCTTGGAGGCTGACATGTGGAGCATTTGGCGTTCATCACTCATCTCTCTGAGC 645

QY      1174  TGCTCATCCCCATTTCGGCGGAGAGTGACCGTGCCACCTCTCTGAACGTCTCTGAGGGG 1233
DB      646  GGAGCGTCCCCATCTCTGGCGGAGACCAAGCAGGAGAGCGTGCAGCAGACATCTCAGCAG 705

QY      1234  CGGTGTATGGAGCAGCCCACTGGGTGCGCACTTCAGCGAAGCAGCCCAAGACTTCATC 1293
DB      706  AACTATGACTTTGATAGGAATATCTTCAGCAGCACACGAGCTGGCCAGGACTTCATC 765

QY      1294  AAGCTACGCTGCAGAGAGCCCTCAGGCCCCGGGCTAGTGGGGCCCAAGTGCTCTCCAC 1353
DB      1294  AAGCTACGCTGCAGAGAGCCCTCAGGCCCCGGGCTAGTGGGGCCCAAGTGCTCTCCAC 1353

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Db 649 CCAGAGATTGTGAACATATGAGCCGCTGGGCTGAGCGGACATGTGAGCATCCGTGTTC 708
QY 1153 ATCTCTACCTCAGCGCTGACCTGCTATCCCAATTTGCCGGGAGAGTGACCTGCGCAC 1212
Db 709 ATCACTATATCTCTGAGGGGTGCATCCCGTTCCTGGGCGAGACCAAGCAGAGAGC 768
QY 1213 CTCTGAAACGCTCTGAGGGGCGGTGTATGAGGAGAGCCCGCCATGGCTGCCACCTCAGC 1272
Db 769 CTCACCAACATCTCAGCGCGTGAATCTACGACTTCGACGAGGAGTACTTACGACACACAGC 828
QY 1273 GAGAGCGCAAGAGCTTCAAGGCTACGCTGACGAGAGCCCTCAGGCGCGGCGCTAGT 1332
Db 829 GAGCTGGGCAAGGAGCTTCAATTCGCGCGCTGCTCAAGATCCCAAGCGGAGATGACC 888
QY 1333 GCGGCCAGTGTCTCTCCACCCCTGGTT 1361
Db 889 ATTGCCAGAGCTTCAACATCTCTGGAT 917
RESULT 7
US-09-186-277-3
; Sequence 3, Application US/09186277
; Patent No. 6171841
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAL, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: 081356/0128
; CURRENT APPLICATION NUMBER: US/09/186.277
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 3
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(1455)
US-09-186-277-3
Query Match 3.3%; Score 173.4; DB 3; Length 2132;
Best Local Similarity 53.3%; Pred. No. 8.1e-26;
Matches 431; Conservative 0; Mismatches 351; Indels 27; Gaps 2;
QY 580 CGGAGAGCTGCACCTCTTCTATGAGTCAAGGAGAGATTGGAAGGGCGGTGTTGGC 639
Db 109 CAGGAGGACGTGGAGGACCATATGAGATGGGAGGAGCTGGCAGCGGCGAGTTGGC 168
QY 640 TTCGTAAGAGAGTGCAGCACAAAGAAACAAGATCTTGTGCTGCCAAGTTTCATCCC- 698
Db 169 ATCGTGGGAAGTGCAGGAGGCAAGGCAAGGAGTACGAGCAAGTTTCATCAAG 228
QY 699 -----CCTACGGAGCAGACTCGGCCCGAGGATACAGGAGCGCA 738
Db 229 AAGCGCCCTGTGATCCAGCGCGGTGGGTGAGCGGAGAGATCGAGCGGAGGTG 288
QY 739 GACATCTGGCGCGCTGAGCACCCCTGCTGACGGGGTGTGAGACAGTTTGAGAC 798
Db 289 AACATCTCTGGGAGATCCGGCACCCCAACATCATCACCTGACGACATCTTCGAGAAC 348
QY 799 CGCAGAGCCCTCATCTCTGAGTGTGCTCATCCGAGAGTGTGAGAGCCCGT 858
Db 349 AAGCGGAGTGTGCTCTGAGTGTGCTCTGCGGGAGGCTCTTGACTTCTCTG 408
QY 859 TACAGAGAGGCGTGGTGCAGGCGCGAGGTCAAGGTCTATCATCAGCAGCTGTGGAG 918
Db 409 GCGGAGAAAGAGTGCCTGACGAGGAGGAGCCACCCAGTTCCTCAAGCAGATCTCGAC 468
QY 919 GSGCTGCATCTGTCAGCAGCCATGGCGTCTCCACCTCGACATAAAGCCCTTCAATC 978

Db 469 GGGCTTCACTACCTGCACTCTAAGCGCATCGCACATTTTGACCTGAAGCGGAACATC 528
QY 979 CTGATGTGTCATCTGCGCGGGAAGAC-----ATTAAATCTGCACTTTGGCTTTGCC 1032
Db 529 ATGCTGTGTCAGCAAGAACGTCGCCAACCCACGAATCAAGCTCATCGACTTCGGCATCGG 588
QY 1033 CAGAACATACCCCGCAGCAGAGCTGAGTTTCAGCCAGTACGGCTCCCTCAGTTCTGTC 1092
Db 589 CACAGATTCAGCGCGGGAACGAGTTCAAGACATCTTGGGACACCCCGAGTTTGGGCC 648
QY 1093 CCCGAGATTCAGCAGCAAGAACCTGTGAGCAAGCCCTCCGACATTTGGGCCCATGGGTGTC 1152
Db 649 CCAGAGATTGTGAATATGAGCGCGCTGGGCTCGAGCGGACATGTGAGAGCATCGGTGTC 708
QY 1153 ATCTCTACCTCAGCGCTGACCTCTCATCCCATTTTCCGCGGAGAGTCAACGTCGAC 1212
Db 709 ATCACTATATCTCTGAGCGGTGCATCCCGTTCCTGGCGGAGACCAAGCAGGAGAGC 768
QY 1213 CTCCTGAACCTCTGAGGCGCGCTGTATGAGCAGAGCCCATGCTGCCACCTCAGC 1272
Db 769 CTCACCAACATCTCAGCGGTGAATCTGAGCGGAGTACTTTCAGCAACACACAGC 828
QY 1273 GAGAGCGCAAGAGCTTCAATTCGCGCGCTGCTCAAGATCCCAAGCGGAGATGACC 888
Db 829 GAGCTGGCAAGGAGCTTCAATTCGCGCGCTGCTCAAGATCCCAAGCGGAGATGACC 888
QY 1333 GCGGCCAGTGTCTCTCCACCCCTGGTT 1361
Db 889 ATTGCCAGAGCTTGAACATCTCTGGAT 917
RESULT 8
US-08-826-267-1
; Sequence 1, Application US/08826267
; Patent No. 5994070
; GENERAL INFORMATION:
; APPLICANT: Streuli, Michel
; TITLE OF INVENTION: No. 5994070el TRIO Molecules and Uses Related Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,267
; FILING DATE: 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,214
; FILING DATE: 27 MARCH (1996)
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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;
; NAME/KEY: CDS
; LOCATION: 67..8647
US-08-826-267-1

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Query Match	2.3%	Score 153.6	DB 2	Length 8906
Best Local Similarity	49.4%	Pred. No. 1.2e-21		
Matches	461	Conservative	0	Mismatches 464; Indels 9; Gaps 2;
QY	435	CTCCCTGGTGCTGAGGCATGTGGCCCTCGAAGGATGCGCGTGTTCACCTGCTGCTGCCCA	494	
DB	7584	CACGCTGAAGATTGTGGGCGTGACACCGAAGATGACGCATCTACACGTGCATGCTGT	7643	
QY	495	AAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTCTTTGGGGGGGACAATGA	554	
DB	7644	CAATGACATGGGTTACGCTCATCATCGGCCACGCTGAGGGTCTTAGTTCAGGGATGA	7703	
QY	555	GCCGGACTCAGAGAAGCAAAAGCCACCGAGGAAGCTGCATCCTCTTATCAGGTCAAGGA	614	
DB	7704	TGGGATCATGGTGACCTGGAAAGAC-----AACTTTGACTCCTCTACAGTGAAGTGC	7757	
QY	615	GGAGATTGGGAAGGGGCGTGTTTGGCTTCGTAAAGAGTGCACACAAAGGAACAGAT	674	
DB	7758	TGAGCTTGGCAGGGGCAAGATTCTCTGTGCTTAAGAAATGTGATCAGAAAGAACCAAGCG	7817	
QY	675	CTTTGCGCTGCCAAGTTTCACTCCCTACCGAGCAGAACTCGGCGCCAGGCATACAGGGA	734	
DB	7818	AGCAGTGGCCACTAAGTTTGTGAACAAGAGTTGATGAAGCGGACAGGTCAACCATGA	7877	
QY	735	GCAGACAATCTTGGCCCGGTGAGCACCCTGCTGCTTAAAGAGTGCACACAAAGGAACAGAT	794	
DB	7878	GCTTGGCATCTCTGACAGACCTTCCAGCACCCCTGCTTGTGCGGCTCTCTCACACCTTTGA	7937	
QY	795	GACCGGAAGACCTCATCTCTCATCTCGAGCTGTGCTCATCCGAGGAGCTGCTGACCG	854	
DB	7938	GACCCCAACAGCTACATCTCTGCTTTAGAAATGGCTGACAGGTCGCTCTCGACTG	7997	
QY	855	CCTGTACAGGAAGCGGTGTGTGACGAGGCGGAGGTCAAGGTCTACATCAGCAGCTGGT	914	
DB	7998	CCTGTGCGATGGGGAAGCCTCACTGAAGGGAAGATCAGGCGCACCTGGGGAGGTTC	8057	
QY	915	GGAGGGCTGCACCTACCTGACACGCCATGGCGTTCTCCACTGGACATAAAGCCCTCTAA	974	
DB	8058	GGAGCTGTCCGTTACCTTGACCACTGCAGATAGACACCTGGACCTAAGCCTGAGAA	8117	
QY	975	CATCCTGATG--GTGCATCTGCCGGGAAGAATTAAATCTGCGACTTTGGCTTTGC	1031	
DB	8118	TATCTGTGGATGAGATTTTAGGCAAGCCAAACCATCAAACTGGCTGACTTTGGAGATGC	8177	
QY	1032	CCAGAACATACCCAGCAGAGCTGCAGTTTCAGCCAGTACGGCTCCCTCGAGTTTCGTCTC	1091	
DB	8178	TGTTCACTCAACAGCACTACTACATCCACAGTTACTGGGGAACCTGAAATTCGCAGC	8237	
QY	1092	CCCGAGATCATCCACAGACACCTGTGAGGAGACCTCCGACATTTGGGGCCATGGTGT	1151	
DB	8238	CCCTGAAATCATCTCTCGGGAACCTCTGCTCGCTGACCTCGGATACGTGGAGTGTGTGAGT	8297	
QY	1152	CATCTCTTACCTCAGCCTGACTGTCTCATCCCAATTTGCCGGCAGAGTGAACCTGGCCAC	1211	
DB	8298	GCTCATACTAGTACTTCTTAGTGGCGTGTCCCTCTTCTGGATGACAGTGTGGAAGAGAC	8357	
QY	1212	CCTCTGAACTGCTGAGGGGCGGTGTATGAGAGAGCCCCATGGCTGCCACCTCAG	1271	
DB	8358	CTGCTGAAACATTTGCCCGTTAGACTTTAGCTTCCAGATGACTACTTTAAAGGAGTGAG	8417	
QY	1272	CGAAGAGCCAAAGACTTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCGCCGCTAG	1331	
DB	8418	CCAGAAGGCCAAGGATTCTGTGTCTTCTCTGAGGAGGACCCCGCAAGCGTCCCTC	8477	
QY	1332	TGCGGCCCATGCTCTCCACCCCTGGTTCCTG	1365	
DB	8478	GGCTGCGCTGGCCCTCCAGAGACAGTGGCTGAG	8511	

RESULT 9
 US-08-878-989-12
 ; Sequence 12, Application US/08878989
 ; Patent No. 5885803
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,989
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PP-0321 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1282 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: PROSNOT06
 ; CLONE: 827431
 US-08-878-989-12

Query Match	2.3%	Score 122.2	DB 2	Length 1282
Best Local Similarity	49.2%	0	Mismatches 329	Indels 0
Matches 319	Conservative			
QY	717	GGCCAGGCATACAGGGAGCGAGACATCCTGGCCGCGCTGAGCCACCGCGTGGTCA	CGG	776
Db	365	GGCCCTGTGGNACGAGATCGCAGTCTCCGTAGGATCAGTCA	CCCCAACATCGTCGC	424
QY	777	GTGTGTGACCAAGTTTGAGACCCGCAAGACCTCATCTCTGAGAGCTGTGTCATC		836
Db	425	TCTGGAGGATGTCCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAACTGGTAC	CGG	484
QY	837	CGAGGAGCTGTGGACCCGCTGTACAGGAAGGGCGTGTGACGGAGCGCGAGGTCA	AGGT	896
Db	485	TGGCAGCTGTGTTGACCCGATCATCTGAGGCGGCTCTCTACACAGAGAAGATGC	CAGCCA	544
QY	897	CTACATCCAGCAGCTGTGTGGAGGGGCTGCATCACTGCACAGCCATGGCGTTC	CCACT	956
Db	545	TCTGTGTGGTCAAGTTCCTTGGCCGCTCTCTACTCTGACAGCCTGGGGAATCGT	CCACCG	604

QY 957 GGACATTAAGCCCTTACATCTGATGCTGCTCCCGGAGACGACATTAATCTG 1016
DB 605 GGACCTTAAGCCCGGAAACCTCTCTGATGCGACGCCCTTTGAGACTCGAGATCATGGT 664
QY 1017 CGACTTTGGCTTTGCCCCAGAACATCACCCAGAGAGCTGAGTTACGCGAGTACGGCTC 1076
DB 665 CTCTGACTTTGAGCTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGAC 724
QY 1077 CCCTGAGTTCTCTCCCGGAGATCATCCAGAGAACCTGTGAGCGAGCTCCGACAT 1136
DB 725 CCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCTTACGGAGGCGCTGATGT 784
QY 1137 TTGGSCCATGGGTGTCTCTCTACTCAGCTGCTGCTCATCCCATTTGCGGCGA 1196
DB 785 GTGGSCCTTGGCGTCACTCTCTATCATCTGTGTGGGTACCCGCCCTTCTACGACGA 844
QY 1187 GAGTGACCGTGGCCACCTCTTGAAGCTCTGGAGGGGGCGGTGTCTGATGGACGACCCAT 1256
DB 845 GAGCGACCTGAGCTCTTTCAGCCAGATCTTGGGGCCAGCTATGAGTTGATNTCTTT 904
QY 1257 GGCCTCCACCTCAGCGAAGACGCCAAAGACTTTCATCAAGGCTACGCTGCGAGAGAGCCCC 1316
DB 905 CTGGGATGACATCTCAGATCAGGCAAGACTTTATTTCGGCACCTTCTGGAGCGAGACCT 964
QY 1317 TGAGCCCGGCTAGTGGGCGGCTGCTCTCCACCCCTGGTTCT 1364
DB 965 TCAGAAGAGGTTACCTGCCAACAGGCTTGGGACCTTTGGATCTT 1012

RESULT 10

US-09-272-796-12
; Sequence 12, Application US/09272796

; Patent No. 6207148

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surya K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/272,796

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/878,989

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

; LENGTH: 1282 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PROSNOT06

; CLONE: 827431

US-09-272-796-12

Query Match 2.3%; Score 122.2; DB 3; Length 1282;

Best Local Similarity 49.2%; Pred No 1.4e-15;

Matches 319; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

QY 717 GGCCGAGGATACAGGAGCGAGACATCTCTGCGCGGTGAGCCACCCGCTGGTACGGG 776
DB 365 GGCCCTGGTGGAGACGAGATCGCATGCTCGGTAGGATCAGTACCCCAACATCGTGC 424
QY 777 GCTGCTGGACCATTTGAGACCGCGCAAGACCTCATCTCTCTGGAGCTTGTCTCATC 836
DB 425 TCTGGAGGATGTCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAATGTTGAGCGG 484
QY 837 CGAGGAGCTGTGGACCGCTGTACAGAGAGGCGGTGTGAGCGAGGCGCGAGGTCAAGT 896
DB 485 TGCGGAGCTGTTGACCGCATCATGGAGCGCGCTCTACACAGAGAGGATGCCAGCCA 544
QY 897 CTACATCCAGAGCTGTTGAGGGGCTGCACTACCTGACAGCCATGGCGTTCACACCT 956
DB 545 TCTGTTGGGTGAGTCTTGGCGCGCTCTCTACCTGACAGCTTGGGATGCTGACCG 604
QY 957 GGACATAAAGCCCTTAACATCTCTGATGTGTCATCTGCGCGGAGACATTAATCTG 1016
DB 605 GGACCTCAAGCCCGAAACCTCTCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGT 664
QY 1017 CGACTTTGGCTTTGCCAGAAATCATACCCAGAGAGCTGAGTTCAGCCAGTACGGCTC 1076
DB 665 CTCTGACTTTGGACTCTCCAAATCCAGGCTGGGAACATGCTAGGACCGCTTGGGAC 724
QY 1077 CCCTGAGTTCTCTCCCGAGATCATCCAGAGAACCTGTGAGCGAGCTCCGACAT 1136
DB 725 CCCTGATATGTGCCCCAGAGCTCTTTGGAGCAGAAACCTTACGGAGGCGGTAGATCT 784
QY 1137 TTGGGCGATGGTGTCT 1196
DB 785 GTGGGCGCTGGGCGTCT 844
QY 1197 GAGTGACCGTGCCACCTCTCTGAACTCTCTGAGGGGCGCTGTCTATGGAGCAGCCCCAT 1256
DB 845 GAGGAGCCCTGAGCTCTTTCAGCCAGATCTCTGAGGCGCAGCTATGAGTTGACNTCTTT 904
QY 1257 GGCTGCCACCTCAGCGAAGAGCGCCAAAGACTTTCATCAAGGCTACGCTGAGAGAGCCCC 1316
DB 905 CTGGGATGACATCTCAGAAATCAGGCAAAAGACTTTATTTCGGCACCTTCTTGGAGCGACCT 964
QY 1317 TCAGGCGCGGCTAGTGGCGGCCAGTGCCTCTCCACCCCTGGTTCT 1364
DB 965 TCAGAAGAGGTTTCACTGCGCAACAGGCTTGGGAGCTTTGGATCTT 1012

RESULT 11

US-09-016-434-953

; Sequence 952, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

QY 1257 GCTGCCCCACCTCAGCGAAGAGCGCAAGAGCTTCAATCAAGCTACGCTGAGAGAGCCCC 1316
DB 905 CTGGGATGACATCTCAGAATCAGGCAAGAGCTTTATTTCGGCACCTTCTGGAGCGAGACCT 964
QY 1317 TCAGCCCGCGCTAGTGGCGCCGAGTGCCTCTCCACCCCTGGTTCCT 1364
DB 965 TCAGAAGAGGTTTCACTGCTCCCAACAGGCGCTTCGGGAGCCTTTGGATCTT 1012

RESULT 12

US-07-951-715A-20

/ Sequence 20, Application US/07951715A

/ Patent No. 5625136

/ GENERAL INFORMATION:

/ APPLICANT: Koziel, Michael G.

/ APPLICANT: Desai, Malini M.

/ APPLICANT: Lewis, Kelly S.

/ APPLICANT: Kramer, Vance C.

/ APPLICANT: Warren, Gregory W.

/ APPLICANT: Evola, Stephen V.

/ APPLICANT: Crossland, Lyle D.

/ APPLICANT: Wright, Martha S.

/ APPLICANT: Merlin, Ellis J.

/ APPLICANT: Launis, Karen L.

/ APPLICANT: Rothstein, Steven J.

/ APPLICANT: Bowman, Cindy G.

/ APPLICANT: Dawson, John L.

/ APPLICANT: Dunder, Erik M.

/ APPLICANT: Pace, Gary M.

/ APPLICANT: Suttie, Janet L.

/ TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

/ TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

/ NUMBER OF SEQUENCES: 94

/ CORRESPONDENCE ADDRESS:

/ ADDRESSES: CIBA-GEIGY Corporation

/ STREET: 7 Skyline Drive

/ CITY: Hawthorne

/ STATE: New York

/ COUNTRY: USA

/ ZIP: 10532

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.0, Version #1.30B

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/07/951,715A

/ FILING DATE: 25-SEP-1992

/ CLASSIFICATION: 800

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/772,027

/ FILING DATE: 04-OCT-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Spruill, W. Murray

/ REGISTRATION NUMBER: 32,943

/ REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (919)541-8615

/ TELEFAX: (919)541-8689

/ INFORMATION FOR SEQ ID NO: 20:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1349 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA

/ HYPOTHETICAL: NO

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 3..1226

/ OTHER INFORMATION: /note= "cDNA sequence for maize

/ OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 953:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-09-016-434-953

Query Match 2.3%; Score 122.2; DB 4; Length 1282;

Best Local Similarity 49.2%; Pred. NO. 1.4e-15;

Matches 319; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

QY 717 GCCCAGCATACAGGAGCGAGCATCTCGCGCGGTGAGCCACCGCTGGTCAAGGG 776
DB 365 GGCCTCTGGGAGACGAGATCGAGTCTCGTAGATCACTACCCACATCTGCTGC 424
QY 777 GCTGCTGACCATTTGAGACCGGCAAGACCTTCATCTCTGAGAGTGTGCTCATC 836
DB 425 TCTGAGGATGTCACAGAGAGCCCTTCCACTCTACCTGGCCATGAACTGTGAGCGG 484
QY 837 CGAGAGCTGTGGACCGCCTGTACAGAGGGCGTGTGACGGAGCGCGAGGTCAAGGT 896
DB 485 TGGCGAGCTGTTGACCGCATCATGGAGCGCGGCTCTTACACAGAGAGGATGCCACCA 544
QY 897 CTACATCCAGCAGCTGGTGGAGGCGCTGCACTACCTGCACAGCCATGGCGTCTCCACCT 956
DB 545 TCTGTTGGTCAAGTCTTGGCGCGCTCTCTACTCTGCACAGCTGGGGATCGTGACCG 604
QY 957 GGACATAAGCCCTCTAACATCTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1016
DB 605 GGACCTCAAGCCCGAAACCTCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGGT 664
QY 1017 CGACTTTGGCTTGGCCAGAACATCACCCAGCAGCTGCGAGTTCAGCCAGTACGGCTC 1076
DB 665 CTCTGACTTTGAGACTCTCAAAATCAAGCTGGGACATGTAGGACCGCGCTTGGAC 724
QY 1077 CCTGAGTTCGCTCCCCGAGATCATCCAGCAGAACCCCTGTGACGAGCCTCCGACAT 1136
DB 725 CCTGGATATGTGGCCCCAGAGCTCTTGAGAGCAGAAACCTACGGAGAGCGCTAGATGT 784
QY 1137 TTGGGCGATGGTGTCTCTCTACTCTAGCTGCTGCTCATCCCATTTGCGGGCA 1196
DB 785 GTGGGCGCTGGGCGTCTCTCTACTCTCTGCTGTGTGAGTACCCCGCTTCTAGACGA 844
QY 1197 GAGTGACCGTGGCCACCGCTCTGAAAGCTCTCTGGAGGGGCGGTGTCTATGAGACGCCCCAT 1256
DB 845 GAGCGACCTTGAGCTCTTTCAGCCAGATCTCTGAGGGCCAGCTATGATGTTGACTTCTCTT 904

OTHER INFORMATION: disclosed in Figure 30."

US-07-951-715A-20

Query Match 2.3%; Score 122.2; DB 1; Length 1349;
Best Local Similarity 51.5%; Pred. No. 1.4e-15;
Matches 333; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 758 GCCACCCGCTGGTCAACGGGGTGTGGACCACTTTGAGACCCGCAAGACCCCTCATCTCA 817
DB 25 GCCACCCCAAGTGTGGGCTCCGGCGCGGTACGAGGACAAGAGCGGTGCACCTCG 84
QY 818 TCCTGGAGCTGTCTCATCCGAGAGCTGTGGACCGCTGTACAGGAAGGGCGTGTGA 877
DB 85 TCATGGAGCTGTGGCGGGGGAGCTCTTCGACCGCATCATCGCCGGGGCCAGTACA 144
QY 878 CGGAGCCGAGGTCAAGGTCTACATCCAGCAGTGTGGAGGGGTGCACTACCTGCACA 937
DB 145 CGGAGCGGGCGCGCGGAGCTGTGGCGGCATCTGTCAGATCGTGCACACCTGCCACT 204
QY 938 GCCATGGGTTCTCCACCTGACATATAAGCCCTCTAACATCTGTATGTCATCTGCC 997
DB 205 CCATGGGGTGTATGACCGGGGACATCAAGCCGAGACTTCTCTGCTGTACGAGAGC 264
QY 998 GGGAG---ACATTAATCTCGGACTTTGGCTTTGGCCAGAACTATCCCCAGCAGAGC 1054
DB 265 AGGACGGCGCCCTCAAGGCCACCGACTTGGGCTCTCCGTCTTCTTCAAGGAGGCGAGC 324
QY 1055 TGCAGTTCCAGCAGTACGGCTCCCTGAGTGTGCTCTCCCGGAGATCATCCAGCAGACC 1114
DB 325 TGCTCAGGACATCGTCGAGCGCCTACTATTCGGCCGAGGTGCTCAAGAGAGT 384
QY 1115 CTGTAGCGAAGCTCCGACATTTGGCCATGGGTGTCTCTACCTCAGCCTGACCT 1174
DB 385 ACG---GCCCGAGGCGGACATCTGGAGCGTCGGCGCTCATCTCTACATCTTCTCGCG 441
QY 1175 GCTCATCCCATTTTCGGGGAGAGTACCGTCCGACCTCTCTGACGCTCTGGAGGGC 1234
DB 442 CGGTGCTTCTTGGGAGAGAACGAGAACGGGATCTTACCGCATCTTCGAGGGC 501
QY 1235 CGGTGTATGAGAGAGCCCATCGCTGCCCATCTCAGCAGAGAGCCAAAGACTTCATCA 1294
DB 502 AGCTTGACCTTCACGAGGAGCCATGGCCACACATCTCGCGGAGGCAAGGATCTGTCA 561
QY 1295 AGGTACGCTGCAGAGAGCCCTCAGCGCGGCTAGTGGGCGGAGTCTCCGAC 1354
DB 562 AGAAGTGTCAATCAATCAACCCAGAGGCGGTACGGGTTTCCAGGTCTCAATCACC 621
QY 1355 CCTGGTCTTGAATCCATCGCTTCGGGAGGAGGCCCACTTTCATCAAC 1401
DB 622 CATGGATCAAGAGAGAGCGGAGCGCGCTGACACGCGGCTTGACAAC 668

RESULT 13

US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."

US-08-459-448A-20

Query Match 2.3%; Score 122.2; DB 2; Length 1349;
Best Local Similarity 51.5%; Pred. No. 1.4e-15;
Matches 333; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 758 GCCACCCGCTGGTCAACGGGGTGTGGACCACTTTGAGACCCGCAAGACCCCTCATCTCA 817
DB 25 GCCACCCCAAGTGTGGGCTCCGGCGCGGTACGAGGACAAGAGCGGTGCACCTCG 84
QY 818 TCCTGGAGCTGTCTCATCCGAGAGCTGTGGACCGCTGTACAGGAAGGGCGTGTGA 877
DB 85 TCATGGAGCTGTGGCGGGGGAGCTCTTCGACCGCATCATCGCCGGGGCCAGTACA 144
QY 878 CGGAGCCGAGGTCAAGGTCTACATCCAGCAGTGTGGAGGGGTGCACTACCTGCACA 937
DB 145 CGGAGCGGGCGCGCGGAGCTGTGGCGGCATCTGTCAGATCGTGCACACCTGCCACT 204
QY 938 GCCATGGGTTCTCCACCTGACATATAAGCCCTCTAACATCTGTATGTCATCTGCC 997
DB 205 CCATGGGGTGTATGACCGGGGACATCAAGCCGAGACTTCTCTGCTGTACGAGAGC 264
QY 998 GGGAG---ACATTAATCTCGGACTTTGGCTTTGGCCAGAACTATCCCCAGCAGAGC 1054
DB 265 AGGACGGCGCCCTCAAGGCCACCGACTTGGGCTCTCCGTCTTCTTCAAGGAGGCGGAGC 324

1055 TCCAGTTCCAGCAGTACCGCTCCCTCCCTGAGTTCTCCCGGAGATCATCCAGCAGAAC 1114
Db TGCTCAGGACATCTCGGAGCGCTTACTACATCGCGCCGAGGTTCTCAAGAGGAGT 384
1115 CTGTGAGGAGACCTCCGACATTTGGCCCATGGTGTCTCTCTCTCTCTCTCTCTCTCT 1174
Db AGC---GCCGAGGCCGACATCTGGAGCGTGGCGTCTCTCTCTCTCTCTCTCTCTCTCT 441
1175 GCTATCCCT 1234
Db GCGTCCCT 501
1235 GCGTGTCTGAGAGCGCCCATGCTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1294
Db AGCTGACCT 561
1295 AGCTGACCT 1354
Db AGAAGATCTCAACATCAACCCCAAGGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 621
1355 CTGTCT 1401
Db CATGATCAAGAGAGCGGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 668

RESULT 14

US-08-459-595A-20
; Sequence 20, Application US/08459595A
; Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8589
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
US-08-459-595A-20

Query Match 2.3%; Score 122.2; DB 3; Length 1349;

Best Local Similarity 51.5%; Pred. No. 1.4e-15;

Matches 333; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 758 GCCACCCGCTGCTCACGGGGCTGTGACCAAGTTTGAGACCGCGCAAGACCTCATCTCTCA 817
Db 25 GCCAGCCCAAGTGTGTGGGCTCCGCGCGGTACGAGGACCAAGCAGCGTGCACCTCG 84
QY 818 TCCTGAGCTGTCTCATCCAGAGAGCTGTGGACCGCTGTACAGAAAGGGCGTGTGA 877
Db 85 TCATGAGCTGTGCGGGCGGGGAGCTCTTCGACCGCATCATCGCCGGGGCGAGTACA 144
QY 878 CGGAGCGCGAGGTCAAGGTCTACATCCAGCAGCTGTGTGGAGGGGCTGCATCTCTCACA 937
Db 145 CGGAGCGCGCGCGCGGAGCTGTGTGGCGCATCTGTGACAGATCGTGCACACCTGCCACT 204
QY 938 GCATGGCGTTCTCCACCTGACATAAAGCCCTCTACATCTCTGAGGGTGCATCTCTGCC 957
Db 205 CCATGGGGTGTGACCGCGGACATCAAGCCCGGAACTTCTGCTGCTCAGCAAGAGCG 264
QY 998 GGGAGAG---ACATTAAATTCGCACTTTGGCTTTGCCAGAAATCATCCCCAGCAGAGC 1054
Db 265 AGGACGCGCGCTCAAGGCCACCGACTTCGCGCTCTCTCTTCAAGGAGGGGAGC 324
QY 1055 TGCAGTTTCAGCAGTACCGCTCCCTGAGTTGGTCTCCCGGAGATCATCCAGCAGAAC 1114
Db 325 TGCTCAGGACATCGTGGCAGCGCTTACTACATCGCGCCGAGGTCTCAAGAGAGT 384
QY 1115 CTGTGAGCAGAGCTTCGACATTTGGGCCATGGGTGTCTCTCTCTCTCTCTCTCTCTCT 1174
Db 385 ACG---GCCCGGAGCGGACATCTGGAGCGTGGCGGTCTCTCTCTCTCTCTCTCTCT 441
QY 1175 GCTCATCCCCATTTGCGGGGAGAGTACCGTGCACCTCTCTGAAACGCTCTGGAGGGGC 1234
Db 442 GCGTCCCTCTCTTCTGGGAGAGAAAGAGAGCGGATCTTCCCGCATCTCTGCGAGGC 501
QY 1235 GCGTGTCTGAGGAGAGCGCCCATGGCTGCCACCTCAGGAGAGCGCAAGAGATTCTATCA 1294
Db 502 AGCTTGACCTCTCCAGGAGAGCCATGGGCCACACATCTGCGCGGAGGCAAGGATCTCTCA 561
QY 1295 AGGCTACGCTCAGAGAGCGCCCTCAGGCCCGGGCTGTGTGGCGCCAGTGCGCTCTCCACC 1354
Db 562 AGAAGATGCTCAACATCAACCCCAAGGAGCGGTCTCAGGGGTTCCAGGTCTCTCAATCACC 621
QY 1355 CCGTGTCTCTGAATTCATCCATCGCTCGGAGGAGCGCCACTTCTATCAAC 1401
Db 622 CATGATCAAGAGAGCGGAGCGGCTCTGACAGCGGCTTGACAC 668

RESULT 15

US-08-459-504B-20

Sequence 20, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Evis, Stephen W.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 36,241
REFERENCE/DOCKET NUMBER: CCI577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-504B-20

Query Match 2.3%; Score 122.2; DB 3; Length 1349;
Best Local Similarity 51.5%; Pred. No. 1.4e-15; Indels 6; Gaps 2;
Matches 333; Conservative 0; Mismatches 308;

QY 758 GCCACCCGCTGGTCAAGGGGCTCTGGACCAAGTTGAGACCCGCAAGACCTCATCTCA 817
DB 25 GCCAGCCCAACGTGGTGGGCTCTCGGGCGGTACGAGGACAAGCAGCGTGCACTCG 84
QY 818 TCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGAGACCGCTGTACAGGAAGGGGCTGTGA 877
DB 85 TCATGGAGCTGTGCGGGGGGGGAGCTCTTTCACCGCATCATCGCCCGGGCCATACA 144
QY 878 CGGAGCGGAGGTCAAGGTCTTACATCAGCAGCTGTGTGAGGGGCTGCTACTCTGACA 937
DB 145 CGGAGCGGCGCGCGCGGAGCTCTGCGGCCATCGTGCAGATCGTGCACACCTGCCACT 204
QY 938 GCCATGCGCTTCTCCACCTGACATAAAGCCCTCTAAATCTGTGATGGTGCATCTCTGCC 997
DB 205 CCATGGGGGTGTCACCCGGGACATCAAGCCCGAGACTTCTGTGCTCAGCAAGGAGC 264
QY 998 GGGAG---ACATTAAATCTGGACTTTGGCTTTGGCTTTGCCAGAACATCAACCCAGCAGAGC 1054
DB 265 AGGACGCGCGCTCAAGGCCACCGACTTGGGCTCTTCCGCTCTTCTTCAAGGAGGGGAGC 324
QY 1055 TGCTAGTTCAAGCAGTACGGCTCCCTGAGTTGCTCTCCCGGAGATCATCCAGCAGAAC 1114
DB 325 TGCTCAGGACATCGTCCGAGCGCTTACTACATCGCGCCCGAGGTCTCAAGAGAGT 384
QY 1115 CTGTGAGCGAAGCTCCGACATTTGGGCGATGGGTGTCTATCTCTACCTCAGCCTGACT 1174
DB 385 ACG---GCCCGGAGGCGGACATCTGGAGGCTCGGCGTCTATCTCTACATCTTCTCGCG 441
QY 1175 GCTCATCCCATTTGCCGGGAGAGTGACGCTGCCACCTCTCTGACGCTCTGGAGGGG 1234
DB 442 GCGTGCTCTCTTCTGGGAGAGAAAGAGACGGCATCTTACCGCCATCTCTCGAGGGG 501
QY 1235 GCGTGTGATGGAGCAGCCCATGGTGGCCACTTACAGGAGAGAGAGAGAGAGAGAGAG 1294
DB 502 AGCTTGACCTCTCCAGCGAGCCATGGGCCACACATCTCGCGGGGAGCCAGGATCTCGTCA 561
QY 1295 AGGCTACGCTGCAGAGAGCCCTCAGCGCGGCTAGTGGCGCCAGTGCGCTCTCCACC 1354
DB 562 AGAAGATGCTCAACATCAACCCCAAGAGGGGCTCAGCGGTTCCAGGTCTCTCAATCACC 621
QY 1355 CTGTGTTCTGAAATCCATGCTGCGGAGAGGCGCCACTTTCATCAAC 1401
DB 622 CATGGATCAAG 668

Search completed: April 26, 2004, 15:05:06
Job time : 248 secs